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| Sequence 22, Application US/10051902 |
| Publication No. US20020178468A1 |
| GENERAL INFORMATION: Steve |
| APPLICANT: Allen, Steve |
| APPLICANT: Hitz, Bill |
| APPLICANT: Tingey, Scott |
| TITLE OF INVENTION: Plant Sugar Transport Proteins |
| TITLE OF INVENTION NUMBER: US/10/051,902 |
| CURRENT FILING DATE: 2002-01-17 |
| PRIOR PELICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/291,922 |
| PRIOR FILING DATE: EARLIER PELICATION NUMBER: GARLIER APPLICATION NUMBER: OS OFTWARE: Microsoft Office 97 |
| SEQ ID NO 2: 30 |
| LENGTH: 510 |
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FBATURE:
NAME/KEY: UNSURE
LOCATION: (102)
  US-10-051-902-22
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                             - protein search, using frame_plus_n2p model
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US-10-051-902-26

Sequence 26, Application US/10051902

Publication No.

Publication No.

APPLICANT: Allen, Steve

APPLICANT: Hitz, Bill

APPLICANT: Tingey, Scott

ITLE OF INVENTION: Plant Sugar Transport Proteins

FILE REFERENCE: BB-163

CURRENT APPLICATION NUMBER: US/10/051,902

CURRENT PILING DATE: EARLIER APPLICATION NUMBER: US/09/291,922

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-14

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Microsoft Office 97

LENGTH: 539

TVPR: DPT
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                                                                  TrpalallevalLeuCys1lePheCys1leMetAlaTyrValAlaPhePheSerIleG1y
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Sequence 26, Application US/10051909

Publication No. US20020199217A1

GENERAL INFORMATION:

APPLICANT: Helentjaris, Tim

APPLICANT: Helentjaris, Tim

APPLICANT: Kinney, Tony

APPLICANT: Tingey, Scott

ITLE OF INVENTION: Plant Sugar Transport Proteins

FILE REFERENCE: Ball 3 US CIP

CURRENT FILING DATE: 2002-01-17

PRIOR APPLICATION NUMBER: US/10/051,909

CURRENT FILING DATE: 2002-01-17

PRIOR APPLICATION NUMBER: 60/083,044

PRIOR PILING DATE: April 24, 1998

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Microsoft Office 97

LENGTH: 539
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| BS Db 426 335 QY 1353 105 OV 1413 | 395 CV 125 Db 145 QV 145 Db 145 OV 515 Db | ## RESULT 5 635 105-10-051-902-28 Sequence 28, Application US/10051902 205 Publication No. US20020178468A1 GENERAL INFORMATION: 695 APPLICANT: Hitz, Bill 225 APPLICANT: Hitz, Bill 225 APPLICANT: Tingey, Tony TITLE OF INVENTION: Plant Sugar Transport Pr FILE REFERENCE: BB-1163 CURRENT APPLICATION NUMBER: US/10/051,902 CURRENT APPLICATION UNDERS: 202-01-17 PRIOR APPLICATION UNDERS: 202-01-17 | 265 872 285 932 305 | 992 Score: 1.55e | 1112 Qy 60 CCAGAGCGAGCCTCCTCTCTCTCTCTCACCACCACC | 45 AlaLeuCysAlaSerMetAlaThrileVal |
|--|---|--|---------------------------------|--|---|--|
| 46 AlaPheAlaCysAlaIleLeuAlaSerMetThrSerIleLeuLeuGlyTyrAspileG1y 65 216 GTGATGAGGGGCGTCGCTACATCAAGAAGGACTTCAACATCAGTGACGGGAAGGTG 27 216 GTGATGAGGGGCGTCGCTACATCAAGAAGGACTTCAACATCAGTGACGGGAAGGTG 27 66 ValMetSerGlyAlaSerLeuTyrIleGlnLysAspLeuLysIleAsnAspThrGlnLeu 85 276 GAGGTTCTCATGGGCATACTGAACCTCTACTCGCTCCTTCGCGGGGGGGG | 336 ACGTCGGACTGGATCGCCGGCGTACACCATCGTGTTCGCCGCCGTCATATTCTTCGCG 106 ThrSerAspTrpIleGlyArgArgPheThrIleValPheAlaAlaValIlePhePheAla 396 GGGSGTTCCTCATGGGGTTCGCCGTCAACTACGCCATGCTCATGTTCGGCCGTTCGTG 126 GlyAlaleulleMetGlyPheSerValAsnTyrAlaMetLeuMetPheGlyArgPheVal 456 GCCGGCATCGGCGTGGCCTACGCCGTCATGTTCGCCGCGTGTCGTG 146 AlaGlyIleGlyValGlyTyrAlaleuMetIleMl | CTGCTCGGGTACGTCCGACTATCTCCCGCTTGCCGCTGAACCTCGGGTGGCGCGCTCCTCGCGTACCTCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCCGCTGCT | 4 1 6 1 4 | GGATCCACTTCTCCAGCATGCGTTGGGCATTCACTCCGTC | | 386 LeuvalGlyLeuAlaThrGlyLeuThrVallleSerArgHisProAspGluLysIleThr |

TACGTCGCCTTCTTCTCCATCGGC 1292 TTCCCGCTCCAGGTGCGCGCGCTG 1352 AGCGGCGTCATCTCCATGACCTTC 1412 TTCTTCCTCTACTCCGGCATCGCC 1472 -----GCCGCCTCGGAATCAGAC 1580 |||:::||||:::||| LysGlnGlyAlaAlaGluAlaAsp 525 CCGGAGATGGCTTCCGCCGCCGCTG 113 AACGTCCGGTTCGCCTTCGCCTGC 167 TACGATATCGGGGTGATGAGCGGG 227 UMBER: US/09/291,922 -14 OGCCACTAAC 1625 ||||||||||| |AlaThrAsn 539 29) ins e U

| Qy 1308 TGGGTGTACAGCTCGGGGTGCGCGCGCTGGGCTGCTCGGCTGGCT | US-10-051-909-28 ISEQUENCE 28, Application US/10051909 SEQUENCE 28, Application US/10051909 PUBLICATION OF US20020199217A1 GENERAL INFORMATION: APPLICANT: Helentjaris, Tim APPLICANT: Hitz, Bill APPLICANT: Hingey, Scott ITILE OF INVENTON: Plant Sugar Transport Proteins FILE REFERENCE: BB163 US CIP CURRENT APPLICATION NUMBER: US/10/051,909 CURRENT FILING DATE: AD202-01-17 PRIOR FILING DATE: April 24, 1998 SOFTWARE: Microsoft Office 97 SEQ ID NO 28 | J.ENGRH. 529 TYPE: PRT ORGANISM: Triticum aestivum US-10-051-909-28 Alignment Scores: Pred. No.: | Oy 60 CCAGAGCGAGCCTCCTCTCTGCACCAGGAGATGGCTTCCGCCGCGTG 113 |
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| 228 GCGTCGCTGAACAACAACTACAACATCAGTGACGGAAGGTCGAGGTTCTCATG 65 AlaSerLeutyrileLysArgAspLeuGln1leThrAspValGlnLeuGluileMethet 84 288 GCGATACTGAACCTCTACTCGCTCATCGCGGCGGGGGGGG | 86 GTCTCGAACTATGCTTTCTCCGGCTTGCCGCTGGACCTCGGGGGCCATCATGCTCGGGGGGGG | 5 ArgGluLeuAspGlyAspValValWalMetProLysThrLysGlyGlyGlyGluGluLysGln 6 GTGTGGAAGGACTCATCCTGTCCCGACCCGGCCATCGCGGCATCCTGTCCGGG | 1068 TTGGTGTCACCAAGAGCTTTTCATCTTGTTGGCCACTTTCTTCATCATCGGG 1127 345 MetGlyValMetLysThrLeuPheIleLeuVallaThrPheGlnLeuAspArgValGly 364 1128 GGGGGCGCTGTTGGTGGCAGCAGGCGGGATAATCCTCTCCTCATCGGCCTGGC 1187 365 ArgArgProLeuLeuLeuThrSerThrAlaGlyMetLeuAlaCysLeuIleGlyLeuGly 384 1188 GCCGGGCTCACCGTGGTGGCAGCAGCAGCCAAGATAATCCTTTGGCCATCGGCCTA 1247 385 ThrGlyLeuThrValValGlyArgHisProAspAlaLysValProTrpAlaIleGlyLeu 404 1248 AGCATCGCCTCACCTTGCTAGCTACGTCTTCTTCTTCATCGGCCTTAGGCCTACAG 1307 1248 AGCATCGCCTCCACCTTAGCTACGTCGCCTTTCTTCTTCATCGGCCTTAGGCCCATCAGG 1307 1258 ThrGlyLeuThrValValGlyArgHisProAspAlaLysValProTrpAlaIleGlyLeu 404 1248 AGCATCGCCTCCACCTTAGCTACGTCGCCTTTCTTCTTCATCGGCCCTTAGGCCCTACAGG 1307 10 |

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                                       CIACTCCGGCATCGCCGCGCTCGCCTGGGTG
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APPLICANT: Allen, Steve
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: B8-116
FURRENT APPLICATION NUMBER: US/10/051,902
CURRENT APPLICATION NUMBER: BALLIER APPLICATION NUMBER: US/09/291,922
PRIOR PRILING DATE: BARLIER FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
LENGTH: 513
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| ::: | 1533 GAGATGAGCAAGCTGTTCGGCGACACGGCCGCGG | Oy 1587 GCCAAGAAGAAGAAGTGGAAATGGCCGCCACT 1622 | RESULT 8 US-10-051-909-20 ; Sequence 20, Application US/10051909 ; Publication No. US20020199217A1 ; GENERAL INFORMATION: | ; APPLICANT: Allen, Steve ; APPLICANT: Helentjaris, Tim ; APPLICANT: Hitz, Bill ; APPLICANT: Vince, Fort | APPLICANT: Tinney, Scott Transport Proteins TITLE OF INVENTION: Plant Sugar Transport Proteins FILE REPERBURGE: BBILGS US CITE FILE REPERBURGE: BBILGS US CITE FILE REPERBURGE: BBILGS US CITE FILE PROTEINS F | CURRENT FILING DATE: 2002-01-17 ; PRIOR APPLICATION NUMBER: 60/083,044 ; PRIOR FILING DATE: April 24, 1998 | | . TYPE: FKI CRGANISM: Zea mays US-10-051-909-20 | Alignment Scores: 2.62e-103 Length: 513 Score: 1872.50 Matches: 372 Percent Similarity: 84.38 Conservative: 60 | ### Match: 13.81% Match: Jidels: | (1.2017) | 1 SECRIBEDIAGE CALCET CONTROL OF SERVICE CANDERS SERVICES OF SERVI | 216 GIGALGAGGGGGGGTGGCTGTACATCAAGAAGACTTCAACATCAGTGAGGGGGGGG | 276 GAGGITCTCAIGGGCAIACTCAACTCTACTCGTCATCGGGCGGGGGGGGGG | 336 ACGTCGGACTGGCCGCGCGCGACCCATCGTGTTCGCCGCCGTCATATTCTTCGCG | 81 ThisseraspargilegiyargargueuthrvalvalPheAlaAlavallePhePhaAlasa. 396 GGGGSGTTCCTCATCGCGTTCGCCGTCAACTACGCCATGCTCATGTTCGCCGCTTCGTG | Db 101 GlySerLeuLeuMetGlyPheAlaValAsnTyrGlyMetLeuMetAlaGlyArgPheVal 120 Qy 456 GCCGGCATCGGGCTACGCGCTCATGATCGCGCCGGTGTACACCGCCGGGGTGTG 515 | |
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| 396 GGGSGTTCCTCATGGGGTTCGCCGTCAACTACGCCATGCTCATGTTCGGCCGCTTCGTG 455 101 GlySerLeuLeuMetGlyPheAlaValAsnTyrGlyMetLeuMetAlaGlyArgPheVal 120 | 1100 | 516 CCGGCGTCGCGCGTGGCTTCCTGACGTCGTTCCGGAGGTGTTCATCAACTTCGGCATC 575 | ω н | 636 ATCATGCTCGGCATCGGCGGCGCGTCCGTGCTGGCGCTCATGGTGCTCGGCATG 695 ::: | 696 CCGGAGTCGCCGCGGTGGTCATCAAQAGACGCCTCGCGGACGCCAAGGTGGTGGTG 755 | 756 GAGAAGACCTCCGACACGGCGCAGGAGCCCCGGGCCCTGGCCGACATCAAGGCCGC 815 | 816 GCCGGCATCCCTGAGGAGCTCCACGGCGACGTGACCGTCCCAAGAGAGGGAGC 872 :: | 873 GGAAACGAGAGGGGGTGTGGAAGGAGCTCATCCTGTCCCCGACCCCGGCCATGCGGGGC 932 | 933 ATCCTGCTGCTGCGGATCGGCATCCAGCTTCCAGCATGGGTTGGGCATTCACTCCGTC 992 | 993 GTCTTCTACAGCCCTCTCGTGTTCAACAGCCCCGGATTAACGAACAACAAAACACTTCTTG 1052 | 1053 GGCACCACTTGGCCGTTCGGTGTCACCAAGAGGCTTTTCATCTTGTTGGTGGCGACTTTCTTC 1112 | 1113 AFCGACGCCGCGCGCCGCTGTTGCTGCGGCACCACGGCGGCATAATCCTCTCC 1172 | 1173 CTCATCGGCCTCGGCCCCGGCCTCACCGTCGCCAGCACCCCCGACGAGATACCT 1232 | 1233 TGGGCCATCGGCCTAAGCATCGCCTCCACCCTCGCCTACGTCGCCTTCTTCTCCATCGGC 1292 | 1293 CTTGGCCCCATCACGTGGGTGTACAGCTCGGAAGATCTTCCGGCTCCAGGTGCGCGCGC | 1353 GGCTGCTCGGCGTCGCCGCCAACCGCGTCACCAGCGGCGTCATCTCCATGACCTTC 1412 ::::: | 1413 CTGTCGCTGTCCAAGGCCATCACCATCGGCGCAGCTTCTTCCTCTACTCCGGCATCGCC 1472 | |

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nd Other Molecules Associated With for Plant Improvement
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Matches:
Conservative:
Mismatches:
Indels:
                                                       Sequence 48931, Application US/10425114
Publication No. US20040034888A1
Fublication No. US2004003488BA1
GENERAL INFORMATION
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Even, Steven E
APPLICANT: Rovalic, David K.
APPLICANT: Cao, Vongwei
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Vongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Oth
TITLE OF INVENTION: Nucleic Acid Molecules and Oth
TITLE OF INVENTION: Nucleic Acid Molecules (CURRENTER APPLICANTON NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
LENGTH: 364
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96.15%
93.68%
50.21%
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ORGANISM: Oryza sativa
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Best Local Similarity:
Query Match:
DB:
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GGCCTCGGCGCCGGGCTCACCGTCGTCGGCCAGCACCCCGACGAGATACCTTGGGCC 1238
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                                            ATCGGCCTAAGCATCGCCTCCACCCTCGCCTACGTCGCCTTCTT
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Matches:
Conservative:
Mismatches:
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Publication No. US20020199217A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Helentjaris, Tim
APPLICANT: Halen, Steve
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Pro
FILE REPERENCE: BEll63 US CIP
FILE REPERENCE: BEll63 US CIP
CURRENT APPLICATION NUMBER: US/10/051,909
CURRENT FILING DATE: 2002-01-17
PRIOR FILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 38
SOFTWARE: MICROSOft Office 97
SEQ ID NO 24
LENGTH: 523
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45.93%
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ORGANISM: Glycine max
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Percent Similarity:
Rest Local Similarity:
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Pred. No.:
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US-10-051-909-24
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.86 ACCICCATCCTCGGCTACGATATCGGGGTGATGAGCGGGGCGTCGCTGTACATCAAG 245
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29 ProProLysArgAsn-----LysPheAlaPheAlaCysAlaThrLeuAlaSerMet
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Mismatches:
Indels:
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                                                                             Length:
Matches:
                                                                       1.95e-86
1589.00
72.23%
61.16%
ORGANISM: Beta vulgaris
                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                            Alignment Scores:
    ; ORGANISM: Bet
US-09-774-381-40
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APPLICANT: MCGARTHY, Sean A.
APPLICANT: MCGARTHY, Sean A.
APPLICANT: Gearing David P.
TITLE OF INVENTION: AND USES THEREFOR
TITLE OF INVENTION NUMBER: 09/010,674
PRIOR PILING DATE: 1999-01-20
PRIOR PILING DATE: 1998-01-20
PRIOR PELING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/014,347
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-12-19
                                                                                                                                                             1418
                                                                               CIGICCAAGGCCATCACCATCGGCGGCAGCTICTTCCTCTACTCCGGCATCGCCGCGCTC 1478
  AICGGCCTAAGCAICGCCTCCACCCTCGCCTACGTCGCCTTCTTCTTCTACGACCTTGGC 1298
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-----AsnGluAsnGlyGlnValAla 513
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|ValGlySerSerIleAlaMetValLeuAlaTyrValAlaThrPheSerIleGlyAlaGly
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Sequence 40, Application US/09774381
Publication No. US20030082677A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
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| Score: 1589.00 Matches: 326 Percent Similarity: 72.23 Conservative: 59 Best Local Similarity: 61.16 Mismatches: 126 Query Match: 43.97 Indels: 22 DB: 5 US-10-051-902A-21 (1-2017) x US-10-051-902-30 (1-549) | Qy 78 TCCTCTGCACCACCGGAGATGGCTTCCGCCGCGCTGCCGGAGGCCGTC 125 | Qy 126 GCGCCGAAGAAGGCCAACGTCCCGGTTCGCCTTCGCCTCCCCTCGCCTCCCTGGCTGGCTTCGCTTCGCCTCCT | Qy 186 ACCICCATCCTCCGGCTACGATATCGGGGGGGGGGGGGGG | Qy 246 AAGGACTTCAACATCAGGGAAGGTGGAGGTTCTCATGGGCATACTGAACTCTAC 305 ::: ::: | Qy 306 TCGCTCATCGGCTCCTTCGCGGGGGGGGGGAACGTCGAACTGGATCGGCCGGC | Qy 366 ATCGTGTTCGCCGCCGTCATATTCTTCGCGGGGGSGTTCCTCATGGGGTTCGCCGTCAAC 425 | Oy 426 TACGCCATGCTCATGTTCGGCCGCTTCGTGGCCGGCATCGGCGCTACGCGCTCATG 485 | Qy 486 ATCGCGCGGTGTACACCGCCGAGGTGTCGCCGCGTCGGCGTGGCTTCCTCACGTCG 545 | Qy 546 TTCCCGGAGGTGTTCATCAACTTCGGCATCCTGCGGGTACGTCTGGACTAGCTTC 605 | Qy 606 TCCGGCTGGAACCTCGGGTGGCGCATCATGCTCGGCATCGGCGGGGCGCGCGC | Qy 666 GTGCTGCGCCTCATGGTGCTCGGCATCGCCGAGTCGCCGCGGTGGTGGTAGAAG 725 :: | Qy 726 GGACGCCTCGCGGACGCCAAGGTGGTGCTGGAGAAGACCTCCGAACACGCGGAGGGCC 785 | Qy 786 GCGGAGCCCTGGCCGACATCAAGGCCGCCGCGGCATCCCTGAGGAGCTCGACGCGAC 845 | Qy 846 GTGGTGACCGTCCCCAAGAGGGGGGGAAACGAGAAGGGGGTGTGGAAGGAGCTCATC 905 ::: | Qy 906 CIGICCCCGACCCCGGCCATGCGGCGCATCCTGCTGCGGGATCGGCATCCACTTCTTC 965 ::: | 966 CAGCATGCGTTGGCCATTCACTCCGTCTTCTACAGCCCTCTCGTGTTCAAGAGCCCC 10: | Db 307 GINGINALaSerGly1leAspAlaValValLeulyrSerFroArgilePneGinSerAla 326 Qy 1026 GGATTAACGAACGACAAACACTTCTTGGCCACCTTGGCCGTTCGGTGTCACCAAGAGG 1085 |
|---|--|---|---|---|--|---|--|---|--|---|---|--|--|---|---|---|--|
| Oy 966 CAGCATGGGTTTGAGTGTTCGTCGTCGTCTTCTACAGCCCTTCGTGTTCAAGAGCCCC 1025 | OY 1086 CTITICATCTIGINGGCAACTITCTTCATCCACGACGCGCGCGCGCGCGTTGCTG 1145 | Qy 1146 GGCAGCACGGGGGATAATCCTCTCCCTCATCGGCCTCGGCGCCGGCTCACGTCGTCTC 1205 | OY 1206 GGCCAGCACCCCAACGCCAAGATACCTTGGGCCATCGGCCTAAGCATCGCCTCCACCCTC 1265 | Qy 1266 GCCTACGTCGCCTTCTTCTCCATCGGCCCCATCACGTGGGTGTACAGCTCGGAG 1325 | Qy 1326 ATCTTCCGGCTCCAGGTGCGCGCTGGGCTGCTCGGCGTCGCGCCAACCGGGTC 1385 ::: | OY 1386 ACCAGCGGCGTCATCCCATGACCTTCCTGTCGCTGTCCAAGGCCATCGGCGGC 1445 | Qy 1446 AGCTTCTTCCTCTACTCCGGCATCGCCGCGCTCGCTGGGTGTTCTTCTACACCTC 1505 ::: | Qy 1506 CCGGAGACCGGCGCCGGACGCTGGAGGAGGAAGCTGTTCGGCGAC 1556 | Oy 1557 ACGGCCGCCGCCGCGAATCAGACGAGCCACC 1589 | Qy , 1590AAGGAGAAGAAGAAGGAAATGGCGCACT 1622 ::: ::: bb 525 AsnGlyAsnAspLysSerGlnValGlnLeuGlyGluThr 537 | RESULT 13 US-10-051-902-30 ; Sequence 30, Application US/10051902 | ; FUDICATION NO. USZUOZUI/8468A1 ; GENERAL INFORMATION: ; APPLICANT: Allen, Steve ; APPLICANT: Hitz, Bill | ; AFFLLCANT: Kinney, Tony ; AFFLLCANT: Tingey, Scott ; TITLE OF INVENTION: Plant Sugar Transport Proteins ; FILE REFERENCE: BB-1163 | CURRENT APPLICATION NUMBER: US/10/051,902 CURRENT FILING DATE: 2002-01-17 PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/291,922 PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-14 | ; NTMAER OF SEQ ID NOS: 30 ; SOFTWARE: Microsoft Office 97 ; SEQ ID NO 30 ; LENGTH: 549 | ; TYPE: PRT ; ORGANISM: Beta vulgaris US-10-051-902-30 | Alignment Scores: Pred. No.: 1.95e-86 Length: 549 |

| 13 13 × 17100-17 + 10-8000-130-04-04-04-04-04-04-04-04-04-04-04-04-04 | USI-902A-ZI (I-ZUI)) X US-10-05I-909-30 (I-S- 78 ICCTCIGCACCGGGGATGGCTTCGGCGGGGGGGGGGGGGG | 126 GCGCCGAAGAAGAGGCCAACGTCCGGTTCGCCTTCGC | Oy 186 ACCTCCATCCTCGGCTACGATATCGGGGTGATGAGCGGGGGTGTTGATGAGGGGGTGATGAAG | | Qy 306 TCGCTCATCGGCTCCTTCGCGGCGGGGGGGACGTCGGACTGGATCGGCCGGGGGGTACACC | 366 | Qy 426 TACGCCATGCTCATGTTCGGCCGCTTCGTGGCCGCGTGGGCTACGCGCTACGCGCTCATG | 486 | 546 | 606 | Qy 666 GTGCTGCTCGTCGTGTTGCTCGGCATGCCGGAGTCGCCGGGTGGCTGGTCATGAAG ::: ::: | Oy 726 GGACGCCTCGCGCACGCCAAGGTGCTGCAGAAGCCTCCGACACGGCGGAGGAGGCCCCCCACACGCGACACGCCCCCC | Oy 786 GCGGAGCCTGGCCAACATCAAGGCCGCCGCCGCGGCATCCCTGAGGAGCTCGACGCGCAC | 846 GTGGTGACCCCCAAQAGAGGGGAAACGAGAAGCGGGTGTGGAAGGAGCTCAT | Db 267 IleTyrLysValGluLysThrLysTleLysSerGlyAsnalaValItpLysGlubeurn 006 CTGTCCGGACCGGACCATGGGGGGGATCCTGCTGCTGCGGGATCGGGATCGACTTCTTC | v 61 | Qy 966 CAGCATGGGTAGGGCATTCACTCCGTCGTCTTCTACAGCCCCTCTGGTGTTCAAGAGCCCC | 1026 | DD 32/ GIVITEINTASHATAARGDVSCIIIDEADAGAINT VAINTAVAIGTVVAINATATATATATATATATATATATATATATATATATATA |
|--|---|--|--|-----|--|------------|--|---|----------------------------------|--|---|---|---|--|--|--|--|--|--|
| | Oy 1086 CTTTCATCTTGTGGCGACTTCTTCATCGACGCGTCGGGCGGCGGCGCGCTGTTGCTG 1145 Db 347 LeuPheileLeuValAlaThrPheGlnLeuAsphysTyrGlyArgArgProLeuLeuLeu 366 | . 1146 GGCAGCACGGGGATAATCCTCTCCCTCATCGGCCTCGGCGCGCGGCTCACCGTCGTC 120 | 126 405 | 132 | CGCGTC 138 Argval 445 | CGGCGC 144 | Qy 1446 AGCTTCTTCCTCTACTCCGGCATCGCCGCGCTCGCTGGGTGTTCTTCTACACCTC 1505 | Qy 1506 CCGGAGACCGGCCGGACGTGGAGAGAGAGCAGCTGTTCGGCGAC 1556 | QY 1557ACGGCCGCCCGCAATCAGACGAGCC | Qy 1590AAGGAGAAGAAGAAGGAGAATGGCCGCCACT 1622 bb s26 AsnGlyAsnAspLysSerGlnValGlnLeuGlyGluThr 538 | RESULT 14 US-10-051-909-30 'Sequence 30, Application US/10051909 'Publication No. US20020199217A1 | GENERAL INFORMATION: APPLICANT: Allen, S APPLICANT: Helentj APPLICANT: Hitz, B | APPLICANT: Kinney, Tony APPLICANT: Tingey, Scott Intle OF INVENTION: Plant Sugar Transport Proteins | CURRENT APPLICATION UNMBER CURRENT FILING DATE: 2007 PRIOR APPLICATION NUMBER: | | SOFTWAKE: MICROSOIC SEQ ID NO 30 LENGTH: 549 | ; TYFE: PKT ; ORGANISM: Beta vulgaris US-10-051-909-30 | Alignment Scores: 1.95e-86 Length: 549 Score: 1589.00 Matches: 326 | Conservative: Mismatches: |

us-10-051-902a-21.rapb

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116 PheLeuMetPheGlyArgPhePheAlaGlyValGlyIleGlyPheAlaPheLeuIleAla
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                                                              TICAACAICAGIGACGGGAAGGIGGAGGIICICAIGGGCAIACIGAACCICIACICGCIC
                                                                                                      GAGGIGITCATCAACTTCGGCATCCTGGGGTACGTCTCGAACTATGCTTCTCCCGC
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            AAGAAGAAGGCCAACGTCCGCTTCGCCTTGCGCCATCCTCGCCTTCCATGACCTCC
                         GluValPheLeuAsnGlyGlyIleLeuIleGlyTyrIleSerAsnTyrGlyPheSerLys
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                                                    372 TICGCCGCCGTCATATICITCGCGGGGGSGTTCCTCATGGGGTTCGCCGTCAACTACGCC
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US-10-425-114-56035

Sequence 56035, Application US/10425114

Publication No. US20040034888A1

Publicant: Number of US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Edou, Yihus

APPLICANT: Screen, Sceen, Steven B

APPLICANT: Cac Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

FILE REFERENCE: 38-21(53313)B

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 56035

LENGTH: 517
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Matches:
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US-10-425-114-56035
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1582.50
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ORGANISM: Glycine max
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Pred. No.:
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Title: Perfect

Sequence:

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Run on:

Scoring table:

Protein e Protein e Protein e

Abu48384 | Abu46992 | Abu31194 |

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Rice, Beta vulgaris-like sugar transport protein, carbohydrate transport, grain filling, annual field crop, plant.
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N-PSDB; ABK51972.
Misc-difference
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   Aau97211 Rice Beta
Abu08336 Rice suga
Aau97213 Wheat sug
Abu08338 Wheat sug
Abu08339 Wheat sug
Abu08339 Wheat sug
Aau97210 Corn Beta
Abu08335 Corn suga
Aau97212 Soybean B
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11397.966 Million cell updates/sec
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                                                                                                                                                                                  Description
                                                                                                June 30, 2004, 18:37:56 ; Search time 100 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                     - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                1586107 segs, 282547505 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Score

Result Š.

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The present invention relates to the isolation of plant polynucleotide sequences encoding an Arabidopsis thaliana-like sugar transport protein or Beta vulgaris-like sugar transport protein. The polynucleotide sequences are useful for altering the level of sugar transport proteins in plants, i.e. for control of carbohydrate transport and distribution in plant cells, e.g. during grain filling of annual field crops (e.g. corn, rice, soybeans, and wheat), and, for studying carbohydrate flows and sugar transport. The polynucleotide sequences can also be used to isolate conn as a sequences and genes that encode homologues of the new proteins. The present sequence represents a rice Beta vulgaris-like sugar transport
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transgenic plants with altered carbohydrate distribution.
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                                                                  Allen SM, Hitz WD, Kinney AJ,
                           17-JAN-2002; 2002US-00051902.
                                   98US-0083044P.
99US-00291922.
                                              (ALLE/) ALLEN S M. (HITZ/) HITZ W D. (KINN/) KINNEY A J. (TING/) TINGEY S V.
                                                                           WPI; 2003-340957/32.
           US2002178468-A1.
   Oryza sativa.
                                   24-APR-1998;
14-APR-1999;
                   28-NOV-2002.
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N-PSDB; ABX93208.

Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein.

Claim 10; Fig 2; 56pp; English.

The present invention relates to the isolation of Arabidopsis thalianalike or Beta vulgaris-like sugar transport proteins, and the polynucleotide sequences encoding them. The plant sugar transport proteins of the invention have been isolated from corn, rice, soybean, and wheat. The polypeptides of the invention may be used for altering the level of expression of a sugar transport protein in a host cell, by transforming a host cell with a chimeric construct encoding all, or a portion of the sugar transport protein, in sense or antisense or institution. Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants. ABU08334-ABU08339 represent Beta vulgaris-like sugar transport proteins

Sequence 510 AA;

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| two ore pomprises | Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: | US-10-051-902A-21 | 96 | ਜ | 156 | 21 | 216 | 41 | 276 | 61 | 336 | 81 | 396 |
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   LeuAlaTrpValPhePheTyrThrTyrLeuProGluThrArgGlyArgThrLeuGluGlu 480
                                                                  500
                                                     ACTGTACACGGCCCAGAGCGA-------GCCTCCTCCTCCTCTGCACCACGGAG
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|ThrGlnGlyGlyProArgArgHisAsnProGlnAlaAlaSerArgGlyAlaSerSerThr
                                     ic acid encoding plant sugar-transport proteins, useful for transgenic plants with altered carbohydrate distribution.
                                                                                                                                                                                                                                                                                                                                                plant
                                                                                                                                                                                                                                                                                                                               Wheat; Beta vulgaris-like sugar transport protein; carbohydrate transport; grain filling; annual field crop;
                                                                                                                                                                                                                                                                                              Wheat sugar transport protein encoded by wlk8.pk0001.all
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N-PSDB; ABK51974.
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like or Beta vulgaris-like sugar transport proteins, and the polynucleotide sequences encoding them. The plant bara transport proteins of the invention have been isolated from corn, rice, soybean, and wheat. The polypeptides of the invention may be used for altering the level of expression of a sugar transport protein in a host cell, by transforming a host cell with a chimeric construct encoding all, or a portion of the sugar transport protein, in sense or antisense or cententation. Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants. ABU08334-ABU08339 represent Beta vulgaris-like sugar transport proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ValMetSerGlyAlaSerLeuTyrIleGlnLysAspLeuLysIleAsnAspThrGlnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the isolation of Arabidopsis thaliana-
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LeuValGlyLeuAlaThrGlyLeuThrVallleSerArgHisProAspGluLysIleThr
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99US-00291922.
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New nucleic acid encoding plant sugar-transport proteins, useful fo
preparing transgenic plants with altered carbohydrate distribution.
                                                                                                                          Example 4; Col 77-80; 54pp; English.
                                                     DUPO ) DU PONT DE NEMOURS & CO
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                                          GGAAACGAGAAGCGGGTGTGGAAGGAGCTCATCCTGTCCCGACCCCGGCCATGCGGCGC
                                                                    ATCCTGCTGTCCGGGATCGGCATCCACTTCTTCCAGCATGCGTTGGGCATTCACTCCGTC
                                                                                               GICTICIACAGCCCTCICGIGIICAAGAGCCCCGGAIIAACGAACGAAACACTICIIG
                                                                                                        LeuvalGlyLeuAlaThrGlyLeuThrValIleSerArgHisProAspGluLysIleThr
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                        GCCGGCATCCCTGAGGAGCTCGACGGCGACGTGGTGACCGTCCCCAAG---AGAGGGAGC
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The present invention relates to the isolation of plant polymucleotide sequences encoding an Arabidopsis thaliana-like sugar transport protein or Beta vulgaris-like sugar transport protein. The polymucleotide sequences are useful for altering the level of sugar transport proteins in plants, i.e. for control of carbohydrate transport and distribution in plant cells, e.g. during grain filling of annual field crops (e.g. contrict, soybeans, and wheat), and, for studying carbohydrate flows and sugar transport. The polymucleotide sequences can also be used to isolate orbs and genes that encode homologues of the new proteins. The present sequence represents a wheat Beta vulgaris-like sugar transport
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GIGGGCTAACGCGCTCAIGAICGCGCCGGTGIACACCGCCGAGGIGICGCCGGCGTCGGGCG 527

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Wheat, Beta vulgaris-like sugar transport protein; carbohydrate transport, grain filling; annual field crop; plant.

Triticum aestivum

Wheat sugar transport protein encoded by wlml.pk0012.hl

(first entry)

27-AUG-2002

us-10-051-902a-21.rag

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The present invention relates to the isolation of Arabidopsis thalianalike or Beta vulgaria-like sugar transport proteins, and the polynucleotide sequences encoding them. The plant sugar transport proteins of the invention have been isolated from corn, rice, soybean, and wheat. The polypeptides of the invention may be used for altering the transforming a host cell, by transforming a host cell with a chimeric construct encoding all, or a portion of the sugar transport protein, in sense or antisense or anticularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants. ABU08334-ABU08339 represent Beta vulgaris-like sugar transport proteins
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505 PheGlyMetThrAspThrAlaValGluAlaGlnAspThrAlaThrLysAspLysAlaLys
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(HITZ/) HITZ W D.
(KINN/) KINNEY A J.
(TING/) TINGEY S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-340957/32.
N-PSDB; ABX93211.
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Query Match:
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14-APR-1999;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 ThrGlyLeuThrValValGlyArgHisProAspAlaLysValProTrpAlaIleGlyLeu 404
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325 ArgValPheGlnSerAlaGlyIleThrGlyAspAsnHisLeuLeuGlyAlaThrCysAla
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                                                                                                                     185 ValSerAsnTyrAlaPheAlaArgLeuProLeuHisLeuSerTrpArgValMetLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta vulgaris-like sugar transport protein; carbohydrate transport; filling; annual field crop; plant.
                                                                                                                                                                                                                 445 ThrSerCysAsnArgValThrSerAlaAlaValSerMetSerPheLeuSerLeuSerLys
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              1188 GCCGGGCTCACCGTCGTCGGCCAGCACCCCGACGCCAAGATACCTTGGGCCATCGGCCTA
                                 385 ThrGlyLeuThrValValGlyArgHisProAspAlaLysValProTrpAlalleGlyLeu
                                                                          CTCCATCGGCCTTGGCCCCCATCACG
                                                                                          405 CysileValSerIleLeuAlaTyrValSerPhePheSerIleGlyLeuGlyProLeuThr
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                             CCGGAG------GCCGTCGCGCCGAAGAAGAAGACGCAACGTCCGGTTCGCCTTCGCCTGC
                                                        ProGluProGlyAlaValHisProArgAsnLysGlyAsnPheLysTyrAlaPheThrCys
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plant sugar transport protein; carbohydrate transport; soybear
carbohydrate distribution; plant.
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plant cells, e.g. during grain filling of annual field crops (e.g. corn, rice, soybeans, and wheat), and, for studying carbohydrate flows and sugar transport. The polynuclectide sequences can also be used to isolate cDNA sequences and genes that encode homologues of the new proteins. The present sequence represents a corn Beta vulgaris-like sugar transport protein
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1872.50
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Best Local Similarity:
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                                                                                                                                                                                                                                                               The present invention relates to the isolation of Arabidopsis thalianalike or Beta vulgaris-like sugar transport proteins, and the polynucleotide sequences encoding them. The plant sugar transport proteins of the invention have been isolated from corn, rice, soybean, and wheat. The polypeptides of the invention may be used for altering the level of expression of a sugar transport protein in a host cell, by transforming a host cell with a chimeric construct encoding all, or a portion of the sugar transport protein, in sense or antisense or intention. Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants. ABU08334-ABU08339 represent Beta vulgaris-like sugar transport proteins
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                                                                                                       Kinney AJ,
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                                                                                                                                                                              Novel plant sugar transport p
protein useful for producing
sugar transport protein.
99US-00291922
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                         ALLEN S M.
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KINNEY A J.
TINGEY S V.
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Query Match:
DB:
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| | Oy 159 Db 32 | 9 TTCGCCTGCGCC/ 2 PheAlaCysAlaM |
| | Qy 219 Db 52 | 9 ATGAGCGGGGGGT |
| | Oy 279 | 9 GTTCTCATGGGC ::: ::: 2 IleLeuLeuGly |
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| s-like sugar transport protein; corn; rice; wheat; transport protein; carbohydrate transport; soybean; distribution; plant. | Db 92 Qy 399 | 2 SerAspTrpileG 9 GSGTTCCTCATGG |
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| sv; | Db 192 | 2 MetLeuGlyvald |
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| Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein. | | |
| | 232 | z nysimiseraspa o ogranocongago |
| present invention relates to the isolation of Arabidopsis thaliana- s or Beta vulgaris-like sugar transport proteins, and the | UY 819 | |
| The plant sugar transport sted from corn, rice, soybean, rice asy he used for altering the | Qy 879 | 9 GAGAAGCGGGTGT |
| t protein in a host cell, by conservict encoding all, or a | Db 271 | 1GluGlyValT |
| portion of the sugar transport protein, in sense or antisense orientation. Particularly, the polypeptides may provide a means to | Qy 939 | 9 CTGTCCGGGATCG |
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|GlyproArgTyrThr11eValPheAlaGlyThr11ePhePheValGly
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                                                                                                                                                                                                                                             GCCTGGGTGTTCTTCTACACCTACCTCCGGGAGACCGCGGCCGGACGCTGGAGGAGATG
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                                                                                                                                                                                                                                                                                                                       ----AsnGluAsnGlyGlnValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                               Linear polyol; mannitol; mannitol transporter; carbon source; plant; pathogen resistance; salt stress; sorbitol; dulcitol; galactitol; inositol; ribitol; xylitol; AgMaT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 of a mannitol transporter designated AgMaT1.
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| GlnValGlnLeuGlyThrAsnVal
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The present sequence represents AgMaT1, which is a transporter of the linear polyol mannitol. DNA encoding the linear polyol is used to produce a selection system for transformed cells, based on the use of polyols as the only carbon source. It is also used to produce transgenic plants with increased resistence to pathogens and salt stress. The use of a linear polyol for selection eliminates the need for toxic selection reagants such as antibiotics. Also, the linear polyol is not essential for the plant, once selection has been made. The linear polyol has a main chain of 5-8, preferably 6, carbon atoms and can also be sorbitol, dulcitol, galactitol, (myo-)inositol, ribitol, or xylitol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 CCGAAGAAGAAGGCCAACGTCCGGTTCGCCTTCGCCTGCGCCATCGTCGCCTCCATGACC 188
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Conservative:
Mismatches:
Indels:
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N-PSDB; ABL41872.
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Query Match:
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99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
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                              Arabidopsis thaliana.
termination sequence
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
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30-APR-1999;
04-MAY-1999;
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11-MAY-1999;
14-MAY-1999;
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24-MAY-1999;
25-MAY-1999;
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14-MAY-1999;
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19-MAY-1
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LysSerHisHisThrGlyHis-----TrpAlaGlyGlyLeuAlaIlePheThrValTyr 390
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               CGCCTCGCGGACGCCAAGGTGCTGGAGAAGACCTCCGACACGGCGGAGGAGGCCGCG 788
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215 ArgLeuGlyGluAlaArgThrValLeuGluLysThrSerThrSerLysGluGluAlaHis
                                                                                                                                                                    451 AlaPheLeuLeuPheAlaValValAlaSerIleGlyTrpValPheMetTyrThrMetPhe
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PR 30-UN-1999, 90US-0140023P.
PR 01-UL-1999, 90US-0141842P.
PR 01-UL-1999, 90US-0141842P.
PR 01-UL-1999, 90US-0141842P.
PR 11-UL-1999, 90US-014203P.
PR 11-UL-1999, 90US-014432P.
PR 11-UL-1999, 90US-014932P.
PR 11-UL-19
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Length:
Matches:
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Mismatches:
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GluAlaValValLeuTyrSerProArg1lePheLysLysAlaG1yValValSerLysAsp
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Katagiri F, Kreps J, Provart N, Ricke D,
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26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
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                                                                            The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a protein conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                AAGAAGAAGGCAACGTCCGGTTCGCCTTCGCCTGCCCATCCTCGCCTCCATGACCTCC 191
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|LeuProValHisLeuSerTrpArgLeuMetPheAlaAlaGlyValValProThrValPhe
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ValGlyAlaLeuLeuAlaGlyTrpThrSerAspArgLeuGlyArgArgLeuThrIleVal
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Matches:
Conservative:
Mismatches:
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                                                             Claim 10; SEQ ID NO 390; 299pp; English
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827.50
48.28%
37.53%
22.90%
                New polynucleotide
reading frame that
resistance, useful
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Best Local Similarity:
Query Match:
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completed: Just 129 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

June 30, 2004, 18:42:55; Search time 24 Seconds (without alignments) 8677.465 Million cell updates/sec nucleic - protein search, using frame_plus_n2p model Run on: ΣO

Title: Perfect score:

BLOSUM62 Scoring table: Sequence:

0.5 7.0 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext 389414 segs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL_frame+ n.Dp. model -DEV=xlp
-MODEL_frame+ n.Dp. model -DEV=xlp
-De_cgnz_1/USFTO_spool_p/USI0051902/runat_30062004_164724_20438/app_query.fasta_1.2183
-DB=LSSued_Patents_AA -QFWT=fastan -SUFFIX=rai -MINWATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=501te -START=1 -ENDS_1 -MATRIX.**Dlosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15
-MODB=LOCAL_OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-DG_V_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPBEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| ! ! ! | , Appl | , Appl | , Appl | , Appl | | , Appl | | , Appl | 11902, A | 11933, A | , Appl | , Appl |
|--------------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|----------------------|----------------------|------------------|------------------|
| Ę : | 22, | 56 | 28 | 20 | 24 | 30 | 18, | | | 11 | 13 | 13 |
| Description | Sequence | Sequence | Sequence | Sequence | Seguence | Seguence | Sequence | Sequence | Seguence | Sequence | Sequence | Sequence |
| D | US-09-291-922-22 | US-09-291-922-26 | US-09-291-922-28 | US-09-291-922-20 | US-09-291-922-24 | US-09-291-922-30 | US-09-291-922-18 | US-10-162-012-46 | US-09-489-039A-11902 | US-09-489-039A-11933 | US-08-928-692-13 | US-09-339-972-13 |
| DB | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 0 | 4 |
| Query Match Length DB | 510 | 539 | | | 523 | 549 | 167 | 488 | 514 | 476 | 584 | 584 |
| Query Match | 71.1 | 55.8 | 52.0 | 51.8 | 45.9 | 44.0 | 18.9 | 18.6 | 16.4 | 16.2 | 15.9 | 15.9 |
| Score | 2570 | 2015 | 1877.5 | 1872.5 | 1660 | 1589 | 682 | 672 | 591 | 585 | 576 | 576 |
| Result No. | | N | ٣ | 4 | 5 | 9 | 7 | 8 | σ | 10 | 11 | 12 |

| sequence 22, Appl | e 2, Appl | e 12, App | e 11731, | e 24, | e 19, App | e 29, | 23, App | 21, | 16, App | 44, App | 8, Appl | 10, App | 10, App | 10, App | 9549, A | 9 | 6, Appl | e, Appl | 5, Appl | 5, Appl | 5, Appl | 3, Appl | m | 11, | 1, | 7 | 463 | 12, | 12, | 4 | 4 |
|-------------------|--------------|-----------------|---------------|---------------|---------------|---------------|---------------|--------------|---------------|--------------|--------------|-------------|--------------|---------------|-------------|-----------------|-------------|-------------|-------------|-------------|-------------|--------------|-------------|--------------|--------------|--------------|--------------|------------|--------------|-----------|------------|
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| | 9-679-686B-Z | -09-679-686B-12 | 09-489-039A-1 | -09-679-686B- | 09-679-686B-1 | 09-291-922-29 | 39-679-686B-2 | J9-679-686B- | 39-679-686B-1 | 10-162-012-4 | 39-291-922-8 | 09-031-392- | 19-299-549-1 | 09-610-417-10 | 39-489-039A | US-09-031-392-6 | 09-299-549- | 09-610-417- | 09-031-392- | 19-299-549- | 09-610-417- | 08-355-844-3 | -0895-16126 | 08-928-692-1 | 09-339-972-1 | 09-291-922-2 | 09-134-001C- | 08-928-69 | 09-339-972-1 | 09-031-39 | 09-299-549 |
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| • | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 2 4 | 25 | 26 | 27 | 28 | 53 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

510 00 00 00 00 WESOLAT 1922-22
Sequence 22 Application US/09291922
Sequence 22 Application US/09291922
Sequence 22 Application US/09291922
GENERAL INPORMATION:
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Tingey, Scott
IIIE COF INVENTION: Plant Sugar Transport Proteins
FILE OF INVENTION: Plant Sugar Transport Proteins
FILE OF INVENTION: Plant Sugar Transport Proteins
FILE REPERENCE: BB-1163
CURRENT APPLICATION NUMBER: 06/083,044
EARLIER APPLICATION NUMBER: 60/083,044
EARLIER FILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
LENGTH: 510
TYPE: PRI
ORGANISM: Oryza sativa Length:
Matches:
Conservative:
Mismatches:
Indels: 3.19e-189 2570.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: NAME/KEY: UNSURE LOCATION: (102) Alignment Scores: Pred. No.:

US-10-051-902A-21 (1-2017) x US-09-291-922-22 (1-510)

| 1236 | Qy 48 ACTGTACACGGCCAGAGCGAGCCTCCTCTCTCTCTCTCTCTCCTCCTCCGGAG 95 |
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| 156 ATGGCTTCCCCCCCCTCCCCCAAGCCCTCCCCCAAACAAA | 1056 ACCACTTGGCCGTTCGGTGTCACCAAGAGGCTTTCATCTTGTTGGCGACTTTCTTCATC 1115 |

| 1293 | 28 Applicat Applicat 383700: Alanayor Allan, St Allan, S | ORGANISM: Triticum aestivum S-09-291-922-28 lignment Scores: | |
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| 46 AlaPheAlaCySAlaIleLeuAlaGerMetThrSerIleLeuLeuGlyTyrAspIleGly 65 216 GTGATGAGCGGGGCTGTCATCATCAAGAAGGATTCAACATCAGTGACGGAAGGTG 275 66 ValMetSerGlyAlaSerLeuTyrIleGlhLysAspLeuLysIleAsnAspThrGlnLeu 85 276 GAGGTTCTCATGGGCATACTGACTCTACTCGCTCCTTGGGGGGGG | 166 ProhlaserAlaArgGlyvalLeuThrSerPheProGluvalPherleAsnPheGlyIle 185 576 CTGCTCGGGTACGTCTCGAACTATGCTTTCTCCGCTTGCCGCTGAACCTCGGGTGGCG 576 CTGCTCGGGTACGTCTCGAACTATGCTTTCTCCGCTTGCCGCTGAACCTCGGGTGGCG 58 ATCATGCTCGGCATCGGCGGCGCGCGCTCCTGCTCGCTCG | GGAAAGGGGGGGGGGAAGGAGTCATCCTGTCCCCGACCCGGCCATCGTCATCGTGGAAGGAGTCATCTGTCCCCGACCCGGCCATCATCATCGTGTGAAGGAGAGACTCATCCTGTCCCCGACCCGGCCATCATCATCATCTTCCTGCTGGATCGGGATCACTTCTTCCAGCATGGGGATTCACTTCAGCATGGGATTCACTTCTACAGCTTGGGGATTCACTTCTACAGGATTAACGAAAGAACACATTCTACAGAACACTTCTACAGAACACTTCTACAGAACACTTCAAGAAGAGACTTAACGAAAACACAAAACACAAAGAAGAAGAATTATCATCTGTTGATGGAACACAACAACAACAACAACAACAACAACAACAACAAC | GIATHTHY ALALA VALUE AND |

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          GCTTCCGCCGCGCTGCCGGTCGCGCCGAAGAAGAAGGGGCAACGTCCGGTTCGCC
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Matches:
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                                                                                           Sequence 24, Application US/09291922
Patent No. 6383776
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Prol
FILE REPRENCE: BB-1163
CURRENT APPLICANTON NUMBER: US/09/291,922
CURRENT APPLICATION NUMBER: 60/083,044
EARLIER APPLICATION NUMBER: 60/083,044
EARLIER PILING DATE: APPLI 24, 1998
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
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; ORGANISM: Glycine max
US-09-291-922-24
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Pred. No.:
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Percent Similarity:
Query Match:
DBs:
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US-09-291-922-24
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| Db 503 LysAlaValGlu | റ സ്പ്രമ | Oy 78 TCCTCTGCACCACCGGAGATGGCTTCCGCCGCTGCCGGAGGCCGTC 125 | Qy 246 AAGGACTTCAACATCAGGAAGGTGGAGGTTCTCATGGGCATACTGAACCTCTAC 305 :: :::: |
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| OY 519 GCGTCGGCGCGGCGTCGTTCCTGACGTTCCTCGGGGTGTTCATCAACTTCGGCATCCTG 578 | | 1119 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGATAATCCTCTCCCTCATC 1178 | 1299 CCCATCACGTGGGTGTACAGCTCGGAGATCTTCCCGCTCCAGGTGCGCGCTGC 1358 409 ProlleThrTrpValTyrSerSerGlullePheProLeuArglaeuhrgAlaGlnGlyAla 428 1359 TCGCTCGGCGCGCCAACCGCGTCACCAGCGCGTCATCCTGTCG 1418 125 TCGCTCGGCGCGCCCAACCGCGTCACCAGCGCGTCATCCTTCTCTCTC |

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ORGANISM: Zea mays
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NAME/KEY: UNSURE
LOCATION: (85)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (98)
FEATURE:
LOCATION: (12)
FEATURE:
LOCATION: (112)
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RESULT 7
US-09-291-922-18
; Sequence 18, Application US/09291922
; Sequence 18, Application US/09291922
; Patent No. 6383776
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
; APPLICANT: Kinney, Tony
; APPLICANT: Kinney, Poott
; TITLE OF INVENTION: Plant Sugar Transport
; TITLE OF INVENTION: Plant
; CURRENT APPLICATION NUMBER: US/09/291,922
; CURRENT FILING DATE: 1999-04-14
; EARLIER PILING DATE: April 24, 1998
; SOFTWARE Microsoft Office 97
; SEQ ID NOS: 30
; SEQ ID NO 18
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| Db 123 LeumetPheGlyArgPheValAlaGlyIleGlyValGlyTyrAlaLeumetIleAlaThr | | Align | Alignment Scores: Pred. No.: |
| .Qy 495 GIGIACACCGCCGAGGIGICGCCGGCGTCGGCGTGGCTICCTGACGTCGTICCCGGAGGGGGGGGGG | CTTCCTGACGTCGTTCCCGGAG 554 | Score: Percer Best I Query | score: Percent Similarity Best Local Similar Query Match: |
| Qy 555 GTGTTCATC 563 | | DB: US-1 | DB: US-10-051-902A-21 |
| Db 163 ValPheile 165 | | ò | 168 GCCA |
| RESULT 8 US-10-162-012-46 | | qq | : 2 AlaL |
| ; Sequence 46, Application US/10162012 ; Patent No. 6682597 | | ζζ | 225 GGGG |
| ; GENERAL INFORMATION: ; APPLICANT: Curtis, Rory A.J. | | qa | 22 GlyP |
| ; APPLICANT: Silos-Santiago, inmaculada ; APPLICANT: Gu, Wei | Ottowar Attived Commonstate | δγ | 273 GTGG |
| ; FILE OF INVESTION: NOVEL HUMAN ION CHANNEL AND INC.; FILE ERFERSES: 10448-19000. | KANSPOKIEK FAMILI MEMBEKS | qu | 42 LeuA |
| CURRENT AFFLICATION NUMBER: US/10/102,012 ; CURRENT FILING DATE: 2002-06-04 | | ζ | 300 CICI |
| ; PRIOR APPLICATION NUMBER: US 60/209,845 ; PRIOR FILING DATE: 2000-06-06 | | qa | 62 LeuG |
| , PRIOR APPLICATION NUMBER: US 09/875,321 , PRIOR FILING DATE: 2001-06-06 | | ζ | 360 TACA |
| , PRIOR APPLICATION NUMBER: PCT/US01/18340 , PRIOR FILING DATE: 2001-06-06 | | qa | : 82 Lyss |
| ; PRIOR APPLICATION NUMBER: US 60/209,257 ; PRIOR FILING DATE: 2000-06-05 | | ò | 420 GTCA |
| ; PRIOR APPLICATION NUMBER: US 09/875,423 ; PRIOR FILING DATE: 2001-06-05 | | qa | 102 ProG |
| ; PRIOR APPLICATION NUMBER: PCT/US01/18398 ; PRIOR FILING DATE: 2001-06-05 | | ò | 456 GCCG |
| | | 1 6 | |
| PRIOR TELLING TOTAL US 09/875,363 | | 1 2 | |
| | | Š 2 | |
| ; PRIOR FILLING DATE: Z001-05-05; PRIOR APPLICATION NUMBER: US 60/227,068 | | <u> </u> | |
| ; PRIOR FILING DATE: 2000-08-22 ; PRIOR APPLICATION NUMBER: US 09/928,530 | | γo | 576 CTGC |
| PRIOR FILING DATE: 2001-08-13 | | qa | 162 Leuv |
| ; PRIOR REFLICATION NOMBER: 5-01/0304/2017); PRIOR FILING PARE: 2000-08-17 | | ζ | 624C |
| PRIOR FILING DATE: 2000-08-21 | | qa | 182 SerT |
| , PRIOR APPLICATION NUMBER: US 09/934,421 ; PRIOR FILING DATE: 2001-08-21 | | ò | 681 ATGG |
| ; PRIOR APPLICATION NUMBER: PCT/US01/26096 ; PRIOR FILING DATE: 2001-08-21 | | q | : 202 GlyL |
| | | ò | 741 GCCA |
| PRIOR APPLICATION NUMBER: US 10/109,029 | | 1 6 | |
| | | } | |
| | | Ž i | |
| ; PRIOR FILING DATE: 2001-05-11 ; PRIOR APPLICATION NUMBER: US (not assigned) | | ପ୍ଧ | 241 GluI |
| DATE: 2002-05-13 | | ò | 861 AAGA |
| ; SOFTWARE FastSEQ for Windows Version 4.0 | | qa | 252 GluG |
| SEC ID NO 46 | | δλ | 918 CCGG |
| TYPE: PRT | | | - |

ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: consensus sequence

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GGCATTCACTCCGTCGTCTTCTACAGCCCTCTCGTGTTCAAGAGCCCCGGATTAACGAAC 1037
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ProlysvalargGlnArgLeuLeuMetGlyValMetLeuGlnAlaPheGlnGlnLeuThr 289
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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| GAGATGGCTTCCGCCGGGGGCCGAGGCCGAAGGAAGAAGGGCAACGTC STATE STATE | 570 GGCATCCTGGGGTACGTCTCGAACTATGCTTTCTCCCGCTTGCCGCTGAACCTCGGG 629 | 750 GTGCTGGAGAAGACCTCCGACACGGCGAGAAGCCCGGAGCGCCTGGCCGACATCAAG 809 [| |
|---|---|---|--|
| 8 4 8 6 8 6 8 6 8 6 8 6 8 6 | 8 & 8 & 8 & | 8 6 8 6 8 6 8 6 | 3 8 3 8 3 |
| Db 290 GlyleAsnAlailePheryrTyrSerProThrilePheLysSerValGlyValSerAsp 309 Oy 1038 GACAACCTCTTGGGCACCTTGGCGTTGCTCACAGAGGCTTTTCATCTTG 1097 310 SerValAlaSerLeuLeuValThrileIleValGlyValValAsnPheValPhrPhe 329 Oy 1098 TTGGGGACTTTCTTCATCGTGGCGGCGGGGGGGGGGTTGCTGGGCAGCAGG 1154 330 ValAlaLeulleHeleuValAphrgPheGlyArghrgProThceuLeulglyAla 349 Oy 1155 GGCGGGATAATCCTCTCCTCCTCATCGGCGGCGGGGGGGTGGTGGTC | | RESULT 8 Sequence 11902, Application US/09489039A TEREACH NO. 6661036 TITLE OF INVENTION: NUGLEC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUGLEC ACID AND THERAPEUTICS FILE REFERENCE: 2709.2004001 TITLE OF INVENTION NUMBER: US/09/489,039A CURRENT PAPLICATION NUMBER: US 60/117,747 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR PLING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 11902 LENGTH: 514 TYPE: PRT CREANISM: Klebsiella pneumoniae US-09-489-039A-11902 | Alignment Scores: 2.85e-37 Length: 514 Fred. No.: 591.00 Matches: 147 Score: 591.00 Matches: 109 Fercent Similarity: 51.82% Conservative: 109 Best Local Similarity: 29.76% Mismatches: 194 Query Match: 16.35% Indels: 194 DB: 4 Gaps: 11 US-10-051-902A-21 (1-2017) x US-09-489-039A-11902 (1-514) |

| 318 TCCTTCGCGGCGGCGGACGTCGGATCGGCCGGTACACCATCGTGTTCGCC 318 ATGTTGCGGGGGGGGGGGGGGGGGGGTACACCACCATCGTGTTCGCG 378 GCCGTCATATTTCTCGCGGGGGGGGGGGTACGCCGTCACTACGCGCTCACTACGCGCTCATCGCGGGGGGGG | Oy 618 CTGAACCTCGGGTGCCCATCATGCTCGGCGCGCGCGCCGTCCTGCTGCTGCGG 677 178 TyrSerGlyAlaTrpArgTrpMetLeuGlyValIleIleIleProAlaUluleuLul Oy 678 CTCATGGTGCTGGCATAGCCGGGGGCGCGGTGTGTGAAGGACGCCTCGCG 737 198 IleGlyValIlePheLeuProAspSerProArgTrpPheAlaAlaLySArgArgPheVal 217 Oy 738 GACGCCAAGGTGCTGGAAAAACCTCCGAACGCGCAGGAGCGCCTCGCG 737 | OY S18 CCGGCCATGCGGCGATCCGGGATCCACTTCTTCCAGCATGCGTTG 977 258 SerAsnPheArgArgAlaValPheLeuGlyIleLeuLeuGlnValMetGlnGlnPheThr 277 OY 978 GGCATTCACTCCGTCTTCTACAGCCCTTCTGTGATCAAGAGCCCGGATTAACGAAC 1037 Db 278 GlyMetAsnVallaMetTyTyTAlaProLysIlePheGluLeuAlaGlyTyTAlaAsn 297 1038 GACAAACACTTCTGGGCCTTGGCGTCTCCAGGGCTTTTCATCTTG 1097 105 ThrThrGluGlnMetTrpGlyThrValileValdlyLeuThrAsnValLeuAlaThrPhe 317 OY 1098 TTGGCGACTTCTTCATCGGCGTCGGGCGCGCGCTTGTGTGGCGTTTTCTTTG 1097 1108 TTGGCGACTTCTTCATCGGCGTCGGGCGGCGGCGCTTTGTTTTTTTT | 1158 GGGATAATCCTCCTCATCGGCGCGGGGGCGGCCGCTCGTCGGCGCCACCGTCGTCGGCGCCGGCTCACGTCGGCCTCACGTCGGCCTCACGTCGGCCTCACGTCGGCTCACGTCGCGCTCACGTCGCTCGC |
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| | ACTION OF THE ACTION OF AC | PRIOR FILING DATE: 1999-01-29 | 0-051-902A-21 (1-2017) x US-09-489-039A-11933 (1-476) 90 CCGGAGATGGCTTCCGCCGGGGGGGGGGCGGGGGGGGGG |

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1140 TIGCIGGGCAGGGGGGGGATAATCCTCTCCCTCATCGGCCTCGGCGCCGGGCTCACC 1199
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423 PheLeuGlyIleLysPheAspGlyAlaValAlaValValValSerSerGlyPheSerSer 442
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LeuLeulleGlyLeuProGlyMetThrMetAlaLeuValValCysSerlleAlaPheHis 422
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|PheAlaGlyThrAlaAlaAspIlePheGlyArgLysArgCysLeuMetGlySerAsnLeu 164
                                                                                                                                                           GGCCGCTTCGTGGCCGGCATCGGCGTGGGCTACGCGCTCATGATCGCGCCGGTGTACACC 503
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GACGGGAAGGTGGAGGTTCTCATGGGCATACTGAACCTCTACTCGCTCATCGGCTCCTTC 323
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LysGluLeuHisThrValProSerAsnLeuArgAlaLeuIleIleGlyCysGlyLeuGln
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                GCGGCCGGGCGGACGTCGGACTCGGCCGGCGGTACACCATCGTGTTCGCCGCCGTC
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| MetPheVallleGlyAlaIleLeuGlnValSerAlaHisThrPheTrpGlnMetAlaVal
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105 GlyTyrileSerSerAlaLeuileSerileGlyThrAspLeuAspHisLysValLeuThr 124
     411 MetileValGlyAlaThrPheLeuThrMetLeuAsnSerLeuGlySerAlaAsnThrPhe 430
                                                                       450
                                                                                                                                                                     Sequence 13, Application US/08928692
Sequence 13, Application US/08928692
Sequence No. 5958727
GENERAL INFORMATION:
APPLICANT: Bansa, Michael
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: A Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587270 No. 5958727disk of No. 5958727th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TICGCCTTCGCCTGCGCCATCCTCGCCTCCATGACCTCCATCCTCCGCCTACGATATC
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                           1512 ACCCGCGGCCGGACGCTGGAGGAGATGAGCAAG 1544
                                                                                                               451 ThrLysAsnValSerLeuGluHisIleGluArg 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGIGTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: No.
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Best Local Similarity:
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Pred. No.:
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US-08-928-692-13
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| Oy 153 TTCGCCTTCGCCTCCTCGCCTCCATGACCTCCATCCTCGGCTACATAT, 212 | | OY 213 GGGGTGATGAGGGGGGGGTGCTGTACATCAAGAACTTCAACATC 260 | 261 | Db 62 TyrAspLysLysGlnMetLysGlySerAlaSerGlnTyrCysLysTyrAspAsnGlnLeu 81 Qy 273 GTGGAGGTTCTCATGGCCATACTGAACCTCTACTGGGTCATCGGCTCCTTCGCGGGGGGGG | Db 82 LeuGliThrPheThrSerSerLeuTyrLeuAlaAlaLeuValSerSerPhePheAlaAla 101 No. 333 CGGACGTGGACTGGATGGCCGGCGGTGATCGTCTTGCCGCCGTCATATTCTTC 392 | 102 ThrValThrArgValValGlyArgLysTrpSerMetPheThrGlyGlyLeuThrPheLeu | Oy 393 GCGGGGGSGTTCCTCATGGGGTTCGCCGTCAACTACGCCATGCTTCGGCCGCTTC 452 | 453 GIGGCCGCATCGCGTGGGCTACGCGCTCATGATCGCGCCGGTGTACACCGCCGAGGTG 5 | | Db 162 AlaProAlaArgLeuArgGlyMetLeuAsnIleGlyPheGlnLeuMetIleThrIleGly 181 Qy 573 ATCCTGGGGTACGTCTCGAACTATGCTTTCTCCCGCTTGCCGCTGAACCTCGGGTGG 632 | 182 | Qy 633 CGCATCATGCTCGGCGCGCGCGCGCTCGTGCTGCTCGCCCTCATGGTGCTCGGC 692 | 693 | Qy 753 CTGGAGAAGACCTCCGACACGGGGAGGAGGCGGGGGGGGG | Oy 813 GCCGCCGGCATCCCTGAGGAGCTCGACGCGACGTGGTGACCGTCCCCAAGAGAGGAGC 872 | OY 873 GGAAACGAGAAGCGGGTGTGGAAGGAGCTCATCCTGTCCCGACCCCGGCCATGCGGCGC 932 | 933 | r 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 1053 | | , , |
|--|------------|---|--------------------------------|--|---|--|--|---|---|---|----------------------|---|---|--|--|--|---|--|---|--|--|
| | CGGGCTCACC | 403 1 | AlavalvalvalSerSerGlyPheSerSer | OY 1233 TGGGCCTAGGCTTAGCATCGCCTCCACGTCGCCTTCTTCTCCATCGC 1292 | 1293 | CATGACCITC | G ThrSerTyrAlaThrAlaThrAsnTrpAlaGlySerLeuVallleAlaSerThrPhe | <pre>Qy 1413 CTGTCGCTGTCCAAGGCCATCACCATCGCGGCACCTTCTTCCTCTACCGGGACTTCTTCTTCTTCGGGGACTTCTTCTTCTTCGGGGGACTTCTTCTTCTTCGGGGGGACTTCTTCTTCTTTCT</pre> | QY 1473 GCGCTCGCCTGGGTGTTCTTCTACACCTACCTCCCGGAGACCCGGGGCCGGACGCTGGAG 1532 | Oy 1533 GAGATGAGCAAGCTGTTCGGCGACACGGCCGCCTCGGAATCAGACGAGCCAGCC | 1593 GAGAAGAAGA 1604 | | AESULT 13 19-69-686B-18 1 Sequence 18, Application US/09679686B 1 Patent No. 662434343 1 Crancos, Inspiration | APPLICANT: Allen, Stephen M. APPLICANT: Lightner, Jonathan B. APPLICANT: Refalski, J. Antoni | TITLE OF INVENTION: HEXOSE CARRIER PROTEINS; FILE REFERENCE: BB1160 US NA; CURRENT APPLICATION NUMBER: 0.5/09/679,686B | PRIOR APPLICATION NUMBER: 60/081,131 PRIOR FILING DATE: 1998-04-09 PRIOR PILING DATE: PRIOR PRIO | FILTUR TALLING DATE: 1393-04-07 FORTHWARE: Microsoft Office 97 SEQ ID NO 18 | ; LENGTH: 517 ; TYPE: PRT ; ORGANISM: Triticum aestivum US-09-679-686B-18 | 4.79e-34 Length: 549.00 Matches: 48 68% Conservative: | est Local Similarity: 29.33% Mismatches: uery Match: 15.19% Indels: 8. | -10-051-902A-21 (1-2017) x US-09-679-686B-18 (1-517) |

| ### STATE OF THE PROPERTY OF T | 362 ILEALAILEGIYALAMETILEGIYVALLYSPheGIYVALAIGIYThrGIyAsnileGIY 381 1209 CAGCACCCCGACGCCAAGATACCTTGGGCCATCGGCCTAAGCATCGCCTCCACCCTCGCC 1268 ::: |
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| LeuvalvalGlyThrLeuIleAlavalLysPheGlyTaACGCCAAGATACCTTGGGCCATCGGCCAAGGATCG LyB | 43 248 63 284 83 |
| Db 363 GlnLeuVal | PhevalThrCysPheileGlyAlaPheGlyGlyLeuilePheGlyTyThspLeuGlyIle PhevalThrCysPheileGlyAlaPheGlyGlyLeuilePheGlyTyThspLeuGlyIle ATGAGCGGGGCGTCGCTGTACATCAAGAAG SerGlyGlyValThrSerMetGluProPheLeuGluGluPhePheProTyrValTyrLys GACTTCAACATCAGT |

| Db 62 OASDValTyrArgArgLysGlnAlaHisLeuHisGluThrAspTyrCysLysTyrAspAs 82 Ov 269 GAAGGTGGAGGTTCTCATG GGCATACTGAACCTCTACGCTCATGGCTCCTTCGC 325 | | 326 GGGGGGGGGGGTGGATGGATGGCCGGGGGTACACCATCGTGTTCGCCGCGGTCAT | Db 102 yalaSerTyrValThrLysArgHisGlyArgArgArgArgArleMetGlyGLyALaAlaSe 122 Qy 386 ATTCTTCGCGGGGGGTTCCTCATGGGGTTCGCGTCAACTACGCCATGCTCATGTTCGG 445 | 14 | | | | 999 | 182 rileGlyileLeuAlaAlaGluLeuIleAsniyrGLyinTAsnuysLleuysAlaGiyl | Oy GGGTGGGGGATCATGGTGGGAATCATGGTGGGGATGGTGGGGGATGATGATGATGATGATGGTGG | 686 GCTCGGCATGCCGGAGTCGCCGCGGTGATCAAAGGACGCCTCGCGAACGAA | | 242 GAIGMCCLECARGARGARGARGARGARGARGARGARGARGARGARGARGA | Db 261 uValAlaAlaSerGluGlu267 | Qy 866 AGGGAGCGGAAACGAGAGCGGGTGTGGAAGGAGCTCATCCTGTCCCCGACCCCGGCCAT 925 | 268 | Oy 926 GGGGGGGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGTGCGGTGTGCTG | Qy 986 CICCGTCGTCTTCTACAGCCCTCTCGTGTTCAAGAGCCCGGGATTAACGAACAAACA | | Oy 1046 CTTCTTGGGCACCACTTGGCCGTTCGGTGTCACCAAGAGGCTTTTCATCTTGTTGGCGAC 1105 :::::: :::::::: | 1106 | | Qy 1161ATAATCCTCTCCCTCATGGCCTGGGGGCTCAGGT 1201 | 360 | Oy 1202 CGFCGGCAGCACCCCGAGGCCAAGAIACCITCGCCATCGCCTCAAGAIACCTGCGCCAGGCCAG | by 1262 CCTCGCCTACGTCGCCTTCTTCTCCCATCGCCCCATCACGTGGGTGTACAGCTC 1321 | Db 396 eCysAlaTyrValAlaGlyPheAlaTrpSerTrpGlyProLeuGlyTrpLeuValProSe 416 |
|--|------------------------|---|---|------|---|-------------------------------|--|--|---|---|---|--|--|-------------------------------|--|---|--|--|---|---|---|------------|--|---|--|---|---|
| 132 | agaggaaga agaggaaga | 435 | Qy 1449 TTCTTCCTCTACTCCGCCATCGCCGCTCGCTGGGTGTTCTTCTACACCTACCT | 1509 | Db 474 GluThrLysAsnValProIleGluGluMetAsnArgValTrp 487 | RESULT 15 US-09-679-686B-2 | ; Sequence 2, Application US/09679686B ; Patent No. 6624343 ; GENERAL INFORMATION: | ; APPLICANT: Allen, Stephen M. ; APPLICANT: Lightner., Onathan E. ; APPLICANT: Rafalski, J. Aatoni | APPLICANT: Thorpe, Catherine J. TITLE OF INVENTION: HEXOSE CARRIER PROTEINS | FILE REFERENCE: BB1160 US NA CURRENT APPLICATION NUMBER: US/09/6 CHIBBENT RILING DATE: 2003-01-16 | PRIOR FILING DATE: 1998-04-09 | ; NUMBER OF SEQ ID NOS: 24 ; SOFUMARE: Microsoft Office 97 ; SEQ ID NO 2 | | | , LOCATION: (488) ; OTHER INFORMATION: Xaa = any amino acid | FEATURE: ; TOTAL/ICE ; TOTAL/ICE: (493) | , OTHER INFORMATION: Xaa = any amino acid US-09-679-686B-2 | 3 Length: | 533.00 Matches: illarity: 48.34% Conservative: | | US-10-051-902A-21 (1-2017) x US-09-679-686B-2 (1-502) | SCAACGTCCG | 4 GlypheGlyGlyGlyGlyAlaAlaAlaGlyArg-AlaGluLeuTyrGluGlyLysIleTh | Oy 152 GTrogecrredecrredecredecredecredecredecredec | 206 COMINICAGGGGGAATGAGGGGGGGGGGGGGGGGGGGGGGGGGGG | | OY 234CTGTACATCAAGAAGGACTTCAACATCAGTGACGG 268 |

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1382 CGTCACCAGGGGGTCATCTCCATGACCTTCCTGTCGCTGTCCAAGGCCATCACCATCGG 1441
                                   436 tPhePheThrPheCys1leAlaGlnAlaPheLeuThrMetLeuCysHisPheLysPhe-- 455
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probable sugar transport protein 205 - beet C:Species: Beta vulgaris (beet) C:Species: Beta vulgaris (beet) C:Species: Beta vulgaris (beet) C:Species: Beta vulgaris (beet) C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000 C:Accession: T14606; T14617

R:Chiou, T.J.; Bush, D.R. Richiou, T.J.; Bush, D.R. Plant Physiol. 110, 511-520, 1996
A;Title: Molecular cloning, immunochemical localization to the vacuole, and expression rittle: Molecular cloning, immunochemical localization to the vacuole, and expression: Patatus: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1549 cHI> A;Residues: 1540 cHI> A;Residues: 1541 cHinnary; translated from GB/EMBL/DDBJ A;Residues: 1541, SVQV, cHI> A;Residues: 1541, SVQV, cHI> A;Residues: 1541, SVQV, cHI> A;Coss-references: EMBL:U64903; NID:g1778094; PID:g1778095 C;Genetics: Darmary ore recent procession: P
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C,Superfamily: glucose transport protein
C,Keywords: sugar transport
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-DE-CORD_2 1/USFTO_spool_p/US10051902/runat_30062004_164723_20424/app_query.fasta_1.2183
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=100 -TRANS=10 -NIGN=15 -NODE=LOCAL
-UNITST=ptc -NORM=ext -HEAPSIZE=500 -MINIB=0 -MAXLEN=200000000
-USER=USI0051902_@CGN 1 1 52 @runat_30062004 164723_20424 -NCPU=6 -ICPU=3
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| & £ | 1326 | ATCTTCC::: | CGCTCC7 | AGGTGCGC | GCGCTGG | SCTGCTC | GCTCGGC | GTCGCCGC | ATCTICCCGCTCCAGGTGCGCGCTGCTCGCTCGCTCGCTCGCCGCCAACCGCGTCTCTCGCTCG | 138 138 448 | <u>s</u> |
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| ço, Qo | 1446 | AGCTTCT | TCCTCT? | ACTCCGGC | ATCGCCG | CGCTCGC ::: lelleal | CTGGGTG aTrpPhe | rrcrrcrad | AGCTTCTTCTACTCCGGCATCGCCGCGCTCGCCTGGGTGTTCTTCTACACCTACCT | C 150 iu 485 | |
| oy Pp | 1506 | CCGGAGA: ProGluT | CCCGCGC hrArgGl | SCCGGACG yArgThrl | CTGGAGG LeuGlua | AGATGAG snMetHi | CAAGCTG ::: sGluLeu | rrcggcgac PheGluAsi | CCGGAGACCGCGCGCGCGCGCGGGGGGGGGGAGGGGGGGG | - 155 p 505 | v |
| Qy Db | 1557 | ArgGluS | erPhePr | ACGGCCGCCGCCTCGGAATCAGACGAGCCAGCCAGCCAGC | GCCTCGG/ LysSerA | AATCAGA ::: snAsnAs; | cgagcca pGluasn | GCC ::: SerThrArg | CC | - 158 r 525 | 6 |
| Qy Db | 1590 | AAGGA :: AsnGlyAsnAs | AGGAGA. ::: snAspLy | AAGGAGAAGAAGGGGAAATGGCGGCCACT ::: ::: ::: ASnASpLySSerGInValGInLeuGlyGluThr | GTGGAAA: :::: ValGlnLe | recccec :: suGlyGl | CACT 162: uThr 538 | 22 8 | | | |
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| Nature 402, 761-768, 1999 A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thalia A,Reference number: A84420; MUID:20083487; PMID:10617197 A,Accession: H84536 A,Status: preliminary | Sequence number of the sequence number of the sequence number of the sequence number of the sequence of the se | 1-768, : nce and mber: A8 84536 iminary | 1999 analys 34420; | is of cl MUID:200 | 1romoson 383487; | ne 2 of PMID:1 | the pl 0617197 | ant Arabi | dopsis t | thalia | ana. |
| A; Molecul A; Residue A; Cross-1 | le typ as: 1- | e: DNA 511 <stc nces: GE</stc |)> 3:AE002 | IIN '860 | 0:946782 | 108; PI | ON: AAD2 | 5954.1; 0 | SPDB:GN0 | 0139 | |
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| Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar Query Match: DB: | Scores Similar | es: rity: ilarity: | 1.42 1579 75.1 60.0 | . 42e-84 5579.00 75.10% 50.00% 13.69% | Leng Matc Cons Misn Inde | Length: Matches: Conservatin Mismatches Indels: | 51 30 77 : 12 | 1 9 1 | | | |
| US-10-051 | -902A | -21 (1- | 2017) x | х н84536 | (1-511) | | | | | | |
| oy Db | 1 1 | ATGGCTTC etAsnSe | cgccgc ::: rsergl | GCTGCCGG ::: yvalGluG | anggccgr Inglyva | CGCG | AlaGlu | erGluPro | AIGGCTTCCGCCGCGCTGCCGAGGCCGTCGCG | G 140 Y 20 | |
| & 90 80 | 141 (| 3GCAACG1 AsnArqSe | CCGGTT :: | CGCCTTCG:: rAlaPheA | CCTGCGC | CATCCTC | GCCTCC AlaSer | TGACCTCC | GGCAACGTCCGGTTCGCCTTCGCCTGCCATCCTCGCCTCCATGACCTCCATCCTCCTCTCTCATCTCTCTC | C 200 | |
| λ | | GGCTACGA | TATCGG | GGTGATGA | GCGGGGG | GTCGCTC | TACATC | AGAAGGAC | GGCTACGATATCGGGGTGATGAGCGGGGGGTCGCTGTACATCAAGAAGGACTTCAACATC | 2 | |

| Db 400 | Db 420 | Qy 1401 | Db 440 | Oy 1461 | Db 460 | Qy 1521 | Db 480 | Qy 1581 | 20 5 40 | RESULT 3 A84537 | probable sug C.Species: A | C;Date: 02-F C;Accession: P:Tin Y K | M.; Koo, H.; | Nature 402, | A;Reference | A;Status: pre A;Molecule ty | A; Cross-refe | C,Genetics: A,Gene: At2g | A;Map positi C;Superfamil | Alignment Sco Pred. No.: | Score: Percent Simil | Best Local S Query Match: | US-10-051-902 | Qy 81 | qq | Oy 143 | Db 20 | Oy 198 | Db 4(| . 258 | 9 qa | Oy 318 | |
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| | AGTGACGGGAAGGTGGAGGTTCTCATGGGCATACTGAACCTCTACTGGCTCATCGGCTCC | serAspValginLeuGlulleLeUMerGlylleLeuAsnilelyserLeu | 321 TTGCGGGGGGGGGGGGGACTGGATTGGATTGGCGGGGGATACCTTGTTTGCGCGGC 380 01 G1.81 all | | GICATATICITICGCGGGGGGGGTTCCTCATGGGGTTCGCCGTCATGCCCATGCTCATG | AlaPhePhePheCysGlyAlaLeuLeuMetGlyPheAlaThrAsnIyrPrOPhelleMet | 441 TTCGGCCGCTTCGTGGCCGGCCGTGGGCTACGCGCTCATGATCGCGCCGGTGTAC 500 | valgiyaigknevalaagiyilediyvaldiyiyialametmedilearariovaliyi | 501 ACGCCGAGGTGTCGCCGGCGTCGGCGTGCCTTCCTGACGTCGTTCCCGGAGGTGTTC 560 14.1 Mh. | THE STATE OF THE S | | 621 AACTICGGGTGGCGCATCATGCTCGGCGATCGGCGGCGGTCCGTGCTGCTGCGCGCTC 680 | ::: | 681 ATGGTGCTCGCCATGCCGGAGTCGCCGCGGTGGTCATGAAGGGACGCCTCGCGGAC 740 | 201 GlyValLeuAlaMetProGluSerProArgTrpLeuValLeuGlnGlyArgLvBF 220 | | 221 AlapheLysValLeuAspLysThrSerAsnThrLysGluGluAlaIleSerArgLeuAsp 240 | | 241 AspileLysArgAlaValGlyIleProAspAspMetThrAspAspValIleValValPro 260 | 861 AAGAGAGGGGGAAACGAGAAGCGGGTGTGGAAGGAGCTCATCCTGTCCCCGACCCCG 920 ::: | 921 GECATAGAGGATCCTGCTGCTGTCCGGATCCGCTTCCACTTCCAGGATGCGTTGGGG 980 | servalargHislleLeulleAlaCysLeuGlylleHisPheAlaGlnGlnAlaSerGly | ATTCACTCCGTCGTCTTCTACAGCCCTCTCGTGTTCAAGAGCCCCGGATTAACGAACG | | AAACACTTCTTGGGCACCACTTGGCCGTTCGGTGTCACCAAGAGGCTTTTCATCTTGTTG 11 | 9 8 8 | GCGACTITCTICATCGACGCGTCGGCGCGCGCGCCGCTGTTGCTGGGCAGCACGGCGGG | 359 | | | 1 GCCAAGATACCTTGGGCCATCGGCCTAAGCATCGCCTCCACCTCGCCTACGTCGCCTTC | Ginini beunysirphiai iegiybeuhiavai iiir vaimet iiir rievaihiii | 1281 THUTHOREFORE THE GOOD THE CANCET CHECK CHAIN CHAIN THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CANCET CHAIN THE CONTROL OF THE CANCET CHAIN THE CANCE |
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11 CGGACGCTGGAGGAGGATGAGCAGAGCTGTTCGGCGACACGCCGCCGCCCCCGCAATCAGAC 1580
                       1 GIBCGCGCGCCTGGCTCGCTCGCCGCCCAACCGCGTCACCAGCGGCGTCATC 1400
                                                                  TCCATGACCTTCCTGTCGCTGTCCAAGGCCATCACCATCGGCGGCAGCTTCTTCCTCTAC 1460
                                    11 TCTGCACCACCGGAGATGGCTTCCGCCGCGCGCCGAGGGCCGTCGCGCCGAAGAAGAAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 GOCAAC---GICCGGTTCGCCTTCGCCTGCGCCTCCATGACCTCCATGCTC 197
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ar transporter [imported] - Arabidopsis thaliana abladopsis thaliana (mouse-ear cress) abladopsis thaliana (mouse-ear cress) [84564] abladopsis thaliana (mouse-ear cress) 684564 [684564] and [684564] 
1517
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TACTOCGGCATCGCCGCGCTCGGGTGTTCTTCTACACCTACCTCCCGGAGACCCGC
                                            3TGTCGCCCGGCGTCGGCCTTCCTGACGTCGTTCGGGAGGTGTTCATCATCATTC
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508 <STO>
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sugar transporter like protein [imported] - Arabidopsis thaliana C;8pecies: Arabidopsis thaliana (mouse-ear cress)
C;Bate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C;Accession: A85433
C;Accession: A85433
A;Rite: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Reference number: A85433
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Residues: 1-493 <STO>
A;Cross_references: GB:NC_001268; NID:97270615; PIDN:CAB80333.1; GSPDB:GN00140
C;Genetics: A74436670
A;Cross_references: GB:NC_001268; NID:97270615; PIDN:CAB80333.1; GSPDB:GN00140
C;Superfamily: glucose transport protein
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120
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1361.00
72.95%
55.53%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Length:
Matches:
Conservative:
Mismatches:
Indels:

3.71e-59 1143.00 65.85% 47.85% 31.63%

transport protein

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A, Map position: 2
C; Superfamily: glucose
                                                                  Percent Similarity:
Best Local Similarity:
Gene: At2g20780
                                       Alignment Scores:
Pred. No.:
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probable sugar transporter [imported] - Arabidopsis thaliana
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 03-Jun-2002
Cisacession: C84593
                                                                              308 ThrThrLysAspLysLeuPheLeu---ValThr1leGlyValGly1leMetLysThrThr
ACCGTCCCCAAGAGAGGGGGGAAACGAGAAGCGGGTGTGGAAGGAGCTCATCCTGTCC
                                          CCGACCCCGGCCCATGCGGCGCATCCTGCTGTCCGGGATCGGCATCCACCTTCTTCCAGCAT
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Rich, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Buss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUD:20083487; PMID:10617197
A; Accession: C84593
A; Ascuts: preliminary
A; Molecule type: DNA
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A; Cross-references: GB:AE002093; NID:94454470; FIDN:AAD20917.1; GSPDB:GN00139
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| 380 CGTCATATICTICGCGGGGGGTICCICAIGGGGTICGCCGTCAACTACGCCAIGCTCAI 439 | | 124 evalGlyArgllePheValGlyPheGljyWalGlyMetAlaSerMetThrSerProLeuTy 144 500 ÇACCGCCGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGAGGTGTT 559 | | | which cost become the control of the cost | 680 CAIGGIGCTGGGCAIGCCGGAGTGGCGGGGGGGTGGTGAIGAAGGGACGCCTCGCGGA 739 ::::::: ::: | 740 CGCCAAGGTGCTGGAGAAGACCTCCGACACGGGGGGGGCCGCGGAGCG 793 :::::: | 794 CCTGGCCGACATCAAGGCCGCCGCCGGCATCCCTGAGGAGCTCGACGGCGACGTGAC 853 | CGTCCCCAAGAGGAAGCGGAACGAGAAGGGGGGGGGG | 911 CCCGACCCCGGCCATGCGGCGCATCCTGCTCGGGATCGGCATCCACTTCTTCCAGCA 970 | TGGGTTGGGCATTCACGCCTCTCTACAGCCCCTGGTGTTCAAGAGCCCGGGATT | 1031 AACGAACGACAAACACTTCTTGGCACCACTTGGCCGTTCGGTGTCACCAAGAGCTTTT 1090 309 *AlaSerashivsThvalaMeralaTeuSerieutTleThrSarGlvieuAshalaTeuGl 329 | CATTOTTOTTGGGACTTTCTTCATCGACGCGCGCGCGCGCGCTGTTGCTGGCAGGCGCGCGC | 1151 CACGGGGGGATAATCCTCTCCCTCATCGGCCTCGGCGCCCGGGGCTCGTCGGCCA 1210 | GCACCCCGACGCCAAGATA | 369 eHisAlaProLysIleAspAlaPheGluSerArgThrPheAlaProAsnAlaThrCysSe 389 | 9 ralaTyrAlaProLeuAlaAlaGluAsnAlaProProSerArgTrpAsnCysMetLysCy | 1230 | 1244 1244 | 429 sValValLeuSerAspAspMetLysAlaThrCysSerSerArgGlyArgThrPhePheLy 449 |
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| | Qy 1272 GTGGCCTTCTTCTCCATGGGCCCCATCAGGGGGGGACAGCTGGAGATCTTC 1331 | Qy 1332 CGGTCCAGGTGCGCGCTGGGCTCGCTCGGCGTCGCCGCCACCGCGTCACCAGC 1391 | OY 1392 GGCGTCATCTCCATGACTTCCTGCGCTGTCCAAGGCCATCGGCGGCAGCTTC 1451 | Oy 1452 TICCTCTACTCCGGCATCGCCGCGCTCTTGTTCTACACCTACCT | 1512 ACCGGGGCGGACGCTGGAGGAGGAGGGAGG 1544 | Db 427 ThrLysGlyArgSerLeuGluGluIleGluGln 437 RESULT 9. | 1yOchetical protein - Arabidopsis thaliana 2;Speches: Arabidopsis thaliana (mouse-ear cress) A;Variety: columbia | ;Date: 03.Aug-1998 #sequence_revision 03.Aug-1998 #text_change 20-Jun-2000 C;Accession: F71431 K;Bevan, M.; Bancroft, I.; Bent, B.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, B.; Wanbutt, R.; Weitzenegder, T.; Pohl, T.M.; Terryn, N.; Giel | avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Aature 391, 485-488, 1998 at the Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech arhoft, A.; Mooree, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ang arhoft, A.; Mooree, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ang | 2.; Chalwarzis, N. AyTitle: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal **Reference number: A71400; MUID:98121113; PMID:9461215 **Accession: F71431 | A;Status: preliminary, nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: 1-582 <bev>A;Cross-references: GB:Z97341; NID:g2244991; PID:g2245004</bev> | ;Genetics: ;Map position: 4C0P9-4G3845 ;Superfamily: glucose transport protein | 3.19e-29 Length: 629.50 Matches: 46.69% Conservat | st Local Similarity: 28.92% Mismatches: ery Match: 17.42% Indels: 2 Gaps: | US-10-051-902A-21 (1-2017) x F71431 (1-582) Qy 149 CCGGTTCGCCTTCGCCTGCGCCATCCTCCATGACCTCCATCCTCCTCGGCTACGA 208 | | Oy 209 TATCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | 269 GAAGGTGGAGGTTCTCATGGGCATACTGAACCTCTACTCGCTCATCGGCTC | DD 04 SLYSIDIIIPDEUGIDSETIDIIEVAIDSETMECALAVALAIAGLYALAIJEVAIGIYAL 84 Qy 32 CTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | |

| | 554 GGTGTTCATCAGCATCCTGGTGGGTACGTCTCGAACTATCCCTTTCCCGGCTT.613 163 yPheLeulleThrGlyGlyGlnPheLeuSerTyrLeulleAnLeulaPheThr 164 GCGGTGAACCTCGGGGGGCGATCGGCGCGCGCGCGCGCGC | 854 CGTCCCCAAGAGGGGGGAAACGAGAAGCGGGTGTGGAAGGAGGCTCATCCTGTCCC 913 251 ulleLeuGluGluGlySerSerGluLysIleAsnMetIleLys | 4 CTGGTGGGCACTTTCTTCACGGGGGGGGGGGGGGGGGGG |
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| Db 427 eserAspAspSerValLysAspLeuCysHisAsnGluAshArgLeuTrpTyThrArgGl 447 Qy 1224AAGATACCTTGGGCCATCGGCTGAGGATGCCTCGCCTGGC 1267 Db 447 yCysProSerAsnPheGlyTrpPheAlaLeuLeuGlyLauGlyLeuGlyLeu |
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| shlaLeuLeuPheValMetValCysValPr 542 3AGCAAGCTG 1547 |
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| rtini, A.M.; Alloni, G.; Azevedo, ' Caldwell, B.; Capuano, V.; Carrer, .D.; Errington, J.; Fabret, C.; Fe |
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| .; Fujita, Y.; Fuma, S.; Galizzi, ., H.; Holsappel, S.; Hosono, S.; H |
| ano, M.; Kurita, K.; Lapidus, A.; .M.; Levine, A.; Liu, H.; Masuda, |
| ark, S.H.; Parro, V.; Pohl, T.M.; B.; Rose, M.; Sadaie, Y.; Sato, T. |
| fone, F.; Sekiguchi, J.; Sekowska, stra, P.; Tognoni, A.; Tosato, V.; |
| mane, K.; Yasumoto, K.; Yata, K.; shikawa, H.; Danchin, A. |
| Gram-positive bacterium Bacillus MID:9384377 |
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| NID:g2636442; PIDN:CAB16017.1; PID |
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| 80 TCCATGACCTCCATCCTCCGCTACGATATCGGGGTGATGAGCGGGGGGTCGCTGTAC 239 |
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AspLeuGlyHisValLeuSerSerGlyGlnLysGluLeuIleThrSerAlaThrSerPhe
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Conservative:
Mismatches:
Indels:
Gaps:
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-557 - ABAD>
A,Cross-references: EMBL:295334; PIDN:CABO8597.1; GS
A,Experimental source: strain 972h-; cosmid c20G8
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C,Superfamily: maltose transport protein MAL61
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| Db 488 PheLeuThrMetMetGluSerIleThrProThrGlyThrPheAlaLeuPheAlaGlyPhe 507 Qy 1470 GCCGCGCTCGCCTGGGTGTTCTTCTACACCTCCCGGAGCCCGGCGCGGCGGCGGTG 1529 iii | SULT 14 4772 babble sugar transporter [imported] - Arabidops Species: Arabidopsis thaliana (mouse-ear crees) Species: Arabidopsis thaliana (mouse-ear crees) Accession: D84772 Lan, X.; Kaul, S.; Rounaley, S.D.; Shea, T.D.; A.Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, T.D.; ss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; ture 402, 761-768, 1999 Accession: D84772 Reference number: A84420; MUID:20083487; PMID:1 Accession: D84772 Anlecule type: DNA Residues: 1-580 <570> Greetius: preliminary Molecule type: DNA Residues: 1-580 <570> Greetius: Arabidops Genetics: Genetics: Genetics: Genetics: Superfamily: glucose transport protein | Alignment Scores: Pred. No.: Pred. No.: Socre: Socre: Socre: Secore: S | Oy 203 CTACGATATCGGGGTGATGAGCGGGCGTCGTACATCAAGAAGGACTTCAACATCGG 262 41 yTyASAINTGLYValileAlaGlyAlaLeuLeuTyIIIelySGluGluPheGlyGluVa 61 52 3 TGACGGAAGGTGGAGGAAGTTCATCGGCATCATCATCGCTCAT 313 51 1 AspasnLysThrTrpLeuGlnGluIleIleValSerMetThrValAlaGlyAlaIleVa 81 61 1 AspasnLysThrTrpLeuGlnGluIleIleValSerMetThrValAlaGlyAlaIleVa 81 62 3 14 CGGCTCTTCGCGGGGGGGGGGTGCTGGTGGTGTGTT 373 63 1 GlyAlaAlaIleGlyGlyTrpTyAsANSpLySPheGlyArgArgMetSerValLeuIl 101 63 4 CGCGCGTCATATTCTTCGCGGGGGGGTTCGTGGTGGTTGGT |

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263 MetLeuLeuGlnAlaMetGlnGlnPheThrGlyMetAsnIleIleMetTyrTyrAlaPro
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| 343 TyrCysLeuMetGlnPheAspAsnGlyThrAlaSerSerGly------
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847089
arabinose-proton symporter - Klebsiella oxytoca
C;Species: Klebsiella oxytoca
C;Species: Klebsiella oxytoca
C;Species: Klebsiella oxytoca
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: 847089
R;Shatwell, K.P.; Charalambous, B.M.; McDonald, T.P.; Henderson, P.J.F.
submitted to the EMBi Data Library, June 1994
A;Description: The nucleotide sequence of the gene araE for arabinose-proton synport in A;Reference number: 847089
A;Reference number: 847089
A;Residues: 1-472 < SHA>
A;Residues: 1-472 < SHA>
A;Cross-references: EMBi:X79598; NID:g498919; PIDN:CAA56110.1; PID:g498920
C;Superfamily: glucose transport protein
C;Keywords: arabinose transport
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    CGTCATCTCCATGACCTTTCCTGTCGCTGTCCAAGGCCATCACCATCGGCGCGCAGCTTCTT 1453
                                                                             CCTCTACTCCGGCATCGCCGCGCTCGCCTGGGTGTTCTTCTACACCTCCCGGAGAC 1513
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LeuGlyArgLysTyrSerLeuMetValGlyAlaValLeuPheValAlaGlySerValGly 105
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ArgGlyLysMet1leSerMetTyrGlnLeuMetValThrLeuGlyIleValMetAlaPhe 165
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-i- PTM: Glycosylated.
-i- SIMILARITY: Belongs to the sugar transporter family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                    gallus gall
chlorella k
zymomonas m
oryctolagus
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neurospora
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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P53387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDILHES 21391710; Who Herisberger J.-D., Chatton J.-Y., Riederer B.M., Thorens B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Stcton myo-inositol co-transporter (Hmit)
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                                                                         HXT2_YEAST
GTR1_CHICK
GTR8_MOUSE
HXT1_YEAST
QAY_NEUCR
GTR3_CHICK
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ZYMMO
RABIT
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RAT
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GTR8_HUMAN
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HXT0_YEAST
KHT2_KLULA
GTR4_HUMAN
GTR3_CANFA
HXT9_YEAST
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GT10 HUMAN
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Genew; HGNC:15956; SLC2A13.
InterPro; IPR007114; MFS.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR005829; Sug_transporter.
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0960E2;
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   NCBI_TaxID=9606;
   RESULT 1
MYCT HUMAN
   Command line parameters:
-MODEL=frame+ n2p.mcdel -DEV=xlp
-MODEL=frame+ n2p.mcdel -DEV=xlp
-MODEL=frame+ n2p.mcdel -DEV=xlp
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-DESA45SPTCC_Spool puery.fasta_1.2183
-DESA45SPTCC_Spool puery.fasta_1.2183
-DESA45SPTCC_STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -TRATS_CORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORN=ext -HEAFSIZE=560 -MINIEN=0 -ARAKEN=200000000
-USRE-USI0051902_GCGN 1 1_22 -GTUNAT 3062004 164722_20400 -NOPU-6 -ICPU=3
-NO MAAP -LARGEQUERY -NEG-SCORES=0 -MAIT -DSPBLCCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADEI -XGAPDC=10 -XGAPBRIT=0.5 -FGAPOP=6
-FGAPERIT=7 -YGAPCP=10 -YGAPCPT=7
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P4633 bacillus su
P4538 klebsiella
P45598 klebsiella
O5273 lactobacill
P09098 escherichia
P30605 escherichia
P30606 escherichia
P30606 escherichia
P30506 eschirolla k
P15729 synechocyst
P15729 synechocyst
P15729 escherillus su
Q10286 echizosacch
Q10286 echizosacch
                                                                                                     June 30, 2004, 18:37:09; Search time 29.5 Seconds (without alignments) 7120.373 Million cell updates/sec
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                                                                                                                                                                                                   Description
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                            protein search, using frame_plus_n2p model
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ITRI YEAST
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ARAE ECOLI
GALL ECOLI
ARAE ARAE
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Maximum Match 1008
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                                                  489 ThralaLeuLeuGlyLeuIleLeuTyrLeuValPhePheAlaProGlyMetGlyProMet
                                                                                                                                                                                                       509 ProfipThrValAsnSerGlulleTyrProLeuTrpAlaArgSerThrGlyAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                    567 GlyLeuLeuPhelleTyrGlyCysLeuProGluThrLysGlyLysLeuGluGluIle
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SEQUENCE FROM N.A.

STRAIN=168 / BGSC1A1;

MEDLINE=$6093926; PubMed=7584049;

Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;

Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita S., Fujimura M., Miwa P., Fujita Y.;

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Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;

Yoshida M., Fujimura M., Fujimura M., Miwa Y., Fujita Y.;

Yoshida M., Fujimura M., Fujimura M., Miwa Y., Fujita Y.;

Yoshida M., Fujimura M., F
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MEDLINE=98044033; PubMed=9384377;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takhashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasarotti A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wippt A., Yamamoto H., Yamane K., Yasumoto K., Yatu K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                      protection function.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                                                                                                                                                                    MEDLINE=99303315; PubMed=10376822; Akbar S. Lee S.Y. Boylan S.A., Price C.W.; Thee S.Y. Boylan S.A., Price C.W.; The scillus subtilis under the sole control of general stress transcription factor sigmaB."; Microbiology 145:1069-1078(1999)
                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Could serve either a nutritional or an osmotic
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| Db 288 IleLeuAsnVallleMetCyi Qy 1134 CCGCTGTTGCTGGCAGCACC Db 308 LysLeuLeuIleTrpGlySe; Qy 1194 CTCACCGTCGTCGGCCAGCA Db 328 LeuLeuThrLeuGlyLeu | | 1314 | Db 383 ValleuSeralaAlaAshLev | 403 | 1494 423 | Oy 1542 AAGCTGTTGGGGGACACGGCC | | SULT 3 22 SCHPO | DT 15-UDL-1998 (Rel. 36, Last second DT 28-FEB-2003 (Rel. 41, Last am DE Myo-inositol transporter 2. | | | | | RC STRAIN=972; RX MEDLINE=21848401; PubMed=11855 RA WOOd V., GWilliam R., Rajandre | | |
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                                                                                                                                                                                                                      STRAIN=PR745;
MEDLINE=98162722; PubMed=9501991;
Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
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EXTRACELLULAR (POTENTIAL).
2 (POTENTIAL).
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EMBL; 295334; CAD8857.1; -
EMBL; 295334; CAD8857.1; -
EMBL; D89225; BAA13913.1; -
PIR; T3125; T38125.

FIR EPPO; EPPO(0114; MES.

IN terPro; IPR00114; MES.

IN terPro; IPR0010828; Sub_transporter.

IN terPro; IPR0010828; Sub_transporter.

IN terPro; IPR0010829; Sub_transporter.

IN terPro; IPR0010829; Sub_transporter.

IN terPro; IPR0010829; Sub_transporter.

PR001083; Sugar_transport.

PR001083; Sugar_tril; I.

IN TIGRORANS; TIGR00849; SP; I.

PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.

PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.

PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NGG.

Transmembrane; Sugar_transport.

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132 AlaAlaLeuIleSerAlaThrThrSerGlyTrpLeuAlaAspTrpValGlyArgLySArg 151
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   10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
11 (POTENTIAL).
12 (POTENTIAL).
12 (POTENTIAL).
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N -> H (IN STRAIN PR745).
N -> H (IN STRAIN PR745).
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M, 20875EC11B153175 CRC64;
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469 489
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9 519
9 557
2 271
4 28
6 61136 MW,
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601.00
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30.13%
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Best Local Similarity:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 GCGTCGCTGTACATCAAGAAGGACTTCAACATCAGTGACGGGAAGGTGGAGGTTCTCATG 287
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-: FUNCTION: Uptake of arabinose across the boundary membrane with the concomicant export of a proton (symport system).
-: SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-: SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT 2; 1.
Transport; Sugar transport; Transport; Transport; Cytoplasmic Pomental).
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InterPro; IRR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005828; Sug_transporter.
InterPro; IPR003863; Sugar_transpt.
InterPro; IPR003863; Sugar_transpt.
Pfam, PP00883; sugar_tri
MEDLINE=95394866; PubMed=7665532;
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338 PheLeuGlnTrpPheGlnGlnPheSerGlyThrAsnAlalleGlnTyrPheSerAlaile 357
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Enterobacteriaceae; Klebsiella.
NCBI_TaxID=571;
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Last annotation update)
orter (Arabinose transporter).
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01-NOV-1995 (Rel. 32, Last seq
28-FEB-2003 (Rel. 41, Last ann
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28-FEB-2003
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374 MetSerAlaAlaProValValTrpIleLeuCysSerGluIleGlnProLeuLysCysArg 393
                                                                                                                                                                                                                                                                                                                                                                                                             the concomitant export of a proton (symport system).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae, Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGKOUGO,;

PROSITE; PS50850; NRS; 1.

PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.

PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.

Transport; Sugar transport; Transmembrane; Symport.

DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).

TANNSMEM 14 34 EXTRACELLULAR (POTENTIAL).
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EXTRACELLUIAR (POTENTIAL)
6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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28-FEB-2003 (Rel. 41, Last annotation update)
D-xylose-proton symporter (D-xylose transporter)
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InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003633; Sugar_transporter.
Pfam; PF00083; sugar_transpt.
                                                                                                                                                            1524 ACGCTGGAGGAGATGAGCAAG 1544
                                                                                                                                                                                ThrieuGluHisIleGluArg 459
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                                 GTGGGCTACGCGCTCATGATCGCGCCGGTGTACACCGCCGAGGTGTCGCCGGCGTCGGCG 527
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                                                                             CGGTGGTGGTCATGAAGGGACGCCTCGCGGACGCCAAGGTGGTGCTGGAGAAGACCTCC 767
ValdíyLeuThrPheMetPheAlaThrPheIleAlaValPheThrValAspLysAladiy 322
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                                                                                                                                                                                                                                   ArgGlyLysMetIleSerMetTyrGlnLeuMetValThrLeuGlylleValMetAlaPhe
                                                   SerSerMetMetLeuGlyAlaAlaIleGlyAlaLeuPheAsnGlyTrpLeuSerPheArg
                                                                                                                        408 ATGGGGTTCGCCGTCAACTACGCCATGCTCATGTTCGGCCGCCTTCGTGGCCGGCATCGGC
                                                                                                                                                                                       126 ValGlyIleAlaSerTyrThrAlaProLeuTyrLeuSerGluMetAlaSerGluAsnVal
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| ArgTrpLeuAlaGluLySGlyArgHisValGluAlaGluGluValLeuArgMetLeuArg
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1347 GCGCTGGGCTCGCTCGGCGTCGCCGCCAACCGCGTCACCAGCGGCGTCATCTCCATG 1406 1407 ACCITICCTGTCGCTGTCCAAGGCCATCACCATCGGCGGCAGCTTCTTCCTCTACTCCGGC 1466 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). ||||||||||:::||| 414 ThrPheLeuThrLeuLeuAspAlaIleGlyAlaAlaGlyThrPheTrpLeuTyrThrAla 433 394 AspPhedlyIleThrCysSerThrThrAsnTrpValSerAsnMetIleIleGlyAla 1467 AIC---GCCGCGCTCGCCTGGGTGTTCTTCTACACCTACCTCCCGGAGACCCGCGGCCGG ::: |||||||||::: 434 LeuAsnValAlaPheIleGlyValThrPheTrp---LeuIleProGluThrLysAsnVal [1] ZEQUENCE FROM N.A. C., Batt C.A., Postma P., Pouwels P., Chaillou S., Bor Y.-C., Batt C.A., Postma P., Pouwels P., Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

| | 1089 TTCATCTTGGGGACTTTCTTC 111. 282 LeualaHisIleGlyIleGlyIlePheAsnValIleValThrAlaIleAlaValAlaIle 301 1113 ATCGACGGGGGGGGGGGGGGGGGGGGGGGGGGGATAATCCTCTCC 117. 1113 ATCGACGGCTCGGGCGGGCGGCTGTTGCTGGGGGGGGGG | qy 1173 cTCATCGGCCTCGGGGTCACCGTCGTCGGCCACCCCGACGCCACCCCAACGCT 1234 | 357 TrpGlyProValMetTrpValMetIleGlyGluValPheProLeuAsnIleArgG 1353 GGCTGGCTGGCGTGCCGCCAACGGGTCACCAGGGGCTCATCATGA 1353 GGCTGGCTCGGCGTCGCCGCCACGGGGTCACCAGGGGGTCATCATGA 137 GlyAsnSerPheAlaSerValIleAsnTrpThrAlaSnMetIleValSerLeuT 1413 CTGTGGGTGTCCAAGGCCATCACGGGGGAGCTTCTTCCTCACTCGGGGA | 397 ProSerLeuLeuAspPhePheGly 1473 GCGCTCGCCTGGGTGTTCTTC 416 CysPheAlaSerIleTrpPheVal 1530 GAGGAGATGAGCAAGCTGTTCGC | 436 1590 451 | ARAE_BCOLI STANDARD; PRT; 472 AA. ID ARAE ECOLI STANDARD; AC P09850; Q46937; DT 01-MAR-1989 (Rel. 10, Created) DT 01-MAR-1989 (Rel. 10, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update) DF Arabinose-proton symporter (Arabinose transporter). GN ARAE OR B2841 OR Z4161 OR ECSA698. | OS Escherichia coli, and OS Escherichia coli, and OS Escherichia coli 0157:H7. OC Bacteria Proteobacteria; Gammaproteobacteria; Enterobacteriales; OC Enterobacteriaceae: Escherichia. OX NCBL TaxID=562, 83334; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=87115869; PubMed=3543693; RA Maiden M.C.J., Davis E.O., Baldwin S.A., Moore D.C.M., |
|--|--|--|---|---|---|--|--|
| FT TRANSMEM 244 264 7 (POTENTIAL). FT DOMAIN 265 280 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 281 301 8 (POTENTIAL). FT DOMAIN 302 309 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 310 330 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 31 337 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 31 337 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 31 370 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 401 11 (POTENTIAL). FT TRANSMEM 401 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 423 457 CYTOPLASMIC (POTENTIAL). FT TOMAIN 423 457 CYTOPLASMIC (POTENTIAL). FT TOMAIN 423 457 CYTOPLASMIC (POTENTIAL). FT SEQUENCE 457 AA, 49199 MW, E097EB2B67A92F67 CRC64; | Alignment Scores: Pred. No.: Pred. No.: Soc.00 Matches: Soc.00 Percent Similarity: 49.80% | 135 AAGAAG 135 AAGAAG 2 ArgLys 195 CTCCTC 195 LeuPhe | CGCTCATC ::::::: lalleLeu TCGTGTTC ::::: | Qy 375 GCCGCCGTCATATTCTTCGCGGGGSGTTCCTCATGGGGTTCGCCGTCAACTACGCCATG 434 | Qy 495 GTGTACACCGCCAGGTGTCGCCGGCGTCGCTCCTGACGTCCTCCCGAG 554 | Oy 615 CCGCTGAACCTCGGCATCATGCTCGGCATCGGCGTCCGTC | Oy 735 GCGGACGCCAAGGTGGTCCTGGAGAACACCTCCGACAGGAGGAGGCGCGG 788 197 AspGlualaArgHisValLeuAspThrMetAsnLysHisAspGlnValalaValAsn 215 Oy 789 GAGCGCTGGCCACATCAAGGCCGCGCGCGCATCCCTGAGGAGCTCGAGGAGGTGGGAGGTG Db 216 LysGlu1leAsnAsp11eGlnGluSerAlaLysIleVal |

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PIR; E85936; E85936.
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SEQUENCE FROM N.A.
STRAIN-0157-117 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PELLMINARY SEQUENCE OF 1-28 FROM N.A.
MEDLINE=84114668; PubMed=6319708;
Stoner C., Schleif R.F.;
Stoner C., Schleif R.F.;
The araE low affinity L-arabinose transport promoter. Cloning, sequence, transcription start site and DNA binding sites of regulatory proteins.,
J. Mol. Biol. 171:369-381(1983).
-!- FUNCTION: Uptake of arabinose across the boundary membrane with the concomicant export of a proton (symptort system).
-!- SUBCELULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Belongs to the sugar transporter family.
                                    sugar transport proteins are homologous.";
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-K12 / MG1655,
BIGLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III. Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
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Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=0157.H7 / EDL933. / ATCC 700927;

MEDLINE=21074935. PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                     STRAIN=K12 / JW2433;
MEDLINE=88228015; PubMed=2836407;
Maiden M.C.J., Jones-Mortimer M.C., Henderson P.J.F.;
Maiden Y.C.J., Sequence, and overexpression of the gene arab coding for arabinose-proton symport in Escherichia coli K12.";
                                                                                                                                                                                                                                              coding for arabinose-proton symporty. Biol. Chem. 263:8003-8010(1988)
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Henderson P.J.F.;
"Mammalian and bacterial
Nature 325:641-643(1987).
                                                                                                              FROM N.A
                                                                                                                 SEQUENCE
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EMBL; U29581; AAB404881; -... EMBL; AE000368; AAC75880.1; -... EMBL; AE005513; AAG57953.1; -... FMBL; AP002563; BAB37121.1; -... PIR; B26430; B26430.

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102 TCCGCCGCGCTGCCGGAGGCCGTCGCGCCGAAGAAGAAGGGCAACGTCCGGTTCGCCTTC 161
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EGGGGGO, SG10056, araE.
InterPro; IPR00114; MFS.
InterPro; IPR00114; MFS.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
Pfam; PR00813; Sugar_tr; 1.
PRINTS; PR00171; SUGAR_RNSPORT.
ITGR?AMS; TIGR00879; SP; 1.
PROSTIE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSTIE; PS00216; SUGAR_TRANSPORT_2; 1.
Transport; Sugar_transport; Transmembrane; Symport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SVA -> YDR (IN REF. 6).
7 411990A441D44393 CRC64;
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5 (POTENTIAL).
PERIPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PERIPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Conservative:
Mismatches:
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Query Match:
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431 TyrThrAlaLeuAsnIleAlaPheValGlyIleThrPheTrp---LeuIleProGluThr 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Dietrich F.S., Mulligan J., Allen B., Araujo R., Aviles E.,
Dietrich F.S., Mulligan J., Cherry J.M., Chung E., Duncan M.,
Huncke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
Suhinart A., Yelton M., Botstein D., Davis R.W.,
Submitted (AUG-1995) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABDUENCE FROM N.A.
MEDLINE=91250431; PubMed=2040626;
Mikawa J.-I., Tsukagoshi Y., Yamashita S.;
Misawa Jation and characterization of two distinct myo-inositol transporter genes of Saccharomyces cerevisiae.";
J. Biol. Chem. 266:11184-11191(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGKUUC.;
PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR TRANSPORT_1; 2.
PROSITE; PS00217; SUGAR TRANSPORT_2; 1.
PROSITE; PS00217; SUGAR TRANSPORT_2; 1.
Transmembrane; Sugar transport; Glycoprotein.
Transmembrane; Sugar transport; Glycoprotein.
DOMAIN 1 (POTENTIAL).
TransNNSMEM 82 102 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: Belongs to the sugar transporter family.
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EXTRACELLULAR (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                       (Rel. 34, Last sequence update) (Rel. 41, Last annotation update)
                                                     1515 CGCGGCCGGACGCTGGAGAGGAGAAGCAAG 1544
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ITR1 OR YDR497C OR D9719.3
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01-OCT-1996 (
28-FEB-2003 (
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-----AlaLeuPheLysIleAsnArgAsnValArgArgAlaValPhe
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| 279 LeualaargalaThrGluValLeuLysArgSerTyrThrAspThrSerGluGluIleIle 789 GAGCGCCTGCCGACCGCCGCCGCCGCACCCTGAGGAGCTCGACGGCGTG 299 GIUALGLYSValiu | Db 383 AsnPhellePheThrLeuValAlaPhePheSerIleAspLySileGlyArgArgThrIle 402 Qy 1140 TTGCTGGCAGCACGGGGGATAATCCTCCCTCATCGGCCTCGGCGGGGTCACC 1199 Db 403 LeuLeuIleGlyLeuProGlyMetThrMetAlaLeuValValCysSerIleAlaPheHis 422 Qy 1200 GTCGTCGGCCAGCACGCCAAGATA | 0y 1233 TGGGCCTAAGCATCGCCTCCACCCTGCCTTCTTCTCCATCGGC 1292 | Db 481 GlyThrSeTTyrAlaThrAlaThrAsnTrpAlaGlySerLeuValileAlaSerThrPhe 500 Qy 1413 CTGTCGCTGTCCAAGGCCATCACGGGGAGCTTCTTCCTCTACTCCGGGATCGCC 1472 | QY 1533 GAGATGAGCTGTTCGGGGCGCCGCCTCGGAATCAGACGAGCCAAG 1592 | Escherichia coli, and Escherichia coli 0157:H7 |
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Sacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Escherichia
NCBI_TaxID=562, 83334;
                                                                                                                                  [6]
SEQUENCE OF 1-192 FROM N.A.
                                                                                                                               DNA Res. 8:11-22(2001)
          SEQUENCE FROM N.A.
                                                 SEQUENCE FROM N.A
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Score:
INDUCTION: BY XYJOSE.

MISCELLANBOUS: E.COLI HAS TWO D-XYLOSE TRANSPORT SYSTEMS THAT ACCUMULATE SUGAR AGAINST A CONCENTRATION GRADIENT: THE XYLE SYSTEM WHICH UTILIZES THE ELECTROCHEMICAL GRADIENT OF PROTONS AND THAT IS INSENSITIVE TO COLD OSMOTIC SHOCK AND THE XYLF SYSTEM THAT USES A HIGH-ENERGY PHOSPHATE COMPOUND AND IS SENSITIVE TO COLD OSMOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Tanaka M., Tobe T., Takami H., Honda T., Sasakawa C., Ogasawara M., Tobe T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
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Nature 325:641-643(1987)
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MEDLINE=21074935; Pubmed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mav B., Glasner J.D.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
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J. Biol. Chem. 262:13928-13932(1987).
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Francoz E., Dassa E.;
"3' end of the malEFG operon in E.coli: localization of the
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12 / MG1655;
MEDLINE=94089392; PubMed=8265357;
Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=87115869; PubMed=3543693;
MEDLING=87115869; PubMed=3543693;
Henderson P.J., Davis E.O., Baldwin S.A., Moore D.C.M.,
Henderson P.J.F.;
                                                                                                     STRAIN=K12;
MEDLINE=88007632; PubMed=2820984;
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SIMILARITY: Belongs to the sugar transporter family.

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Complete proteome. Symport; Transmembrane; Inner membrane; Symport; DOMAIN COMPLET (POTENTIAL).
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EMBL, AE00536; AAC59230.1; -
EMBL, AE00568; BAB38437.1; -
EMBL, AP02568; BAB38437.1; -
EMBL, AP0648; CAR2986; Incerpro; IPR005829; Sug_transporter.
Incerpro; IPR005829; Sug_transporter.
Incerpro; IPR005829; Sug_transporter.
Incerpro; IPR005829; Sug_transporter.
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| δλ | AACGAGAAGCGGGTGTGGGAAGGAGCTCATCCTGTCCCCGACCCCGGCCATGCGGC | | irts P.E.; is (1992), Unive |
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| ζζ | 0- | | INE=97426617; Put |
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| ò | | | or J., Davis N.W. B., Shao Y.; |
| ପୁପ | 291 ValGlyIleAsnValValLeuTyrTyrAlaProGluValPheLysThrLeuGlyAlaSer 310 | | complete genome nce 277:1453-1474 |
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| đ | 311 ThrAspileAlaLeuLeuGlnThrileIleValGlyValileAsnLeuThrPheThr 329 | | INE=22388234; Put |
| δγ | | | Welch K.A., Burland v Rasko D., Buckles E.I |
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| δλ | GGCGGGAT | | Excensive mosaic ser of uropathogenic Esch Proc. Natl. Acad. Sci |
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; PubMed=12471157;
and V., Plunkett G. III, Redford P., Roesch P.,
e D.J., Zhou S.-R., Boutin A., Hackett J., Stroud D.,
e D.J., Zhou S., Schwartz D.C., Perna N.T.,
connenberg M.S., Blattner F.R.;
c structure revealed by the complete genome sequence
Escherichia coli.;
sci. U.S.A. 99:17020-17024 (2002).
TAKE OF GALACTOSE ACROSS THE BOUNDARY MEMBRANE WITH
ANT EXPORT OF A. PROTON (SYMPORT SYSTEM).
LOCATION: Integral membrane protein. Inner membrane.
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kett G. III, Bloch C.A., Perna N.T., Burland V.,
ides J., Glasner J.D., Rode C.K., Mayhew G.F.,
W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGCGCCATCCTCGCCTCCATGCCTCCTCGGCTACGATATCGGGGTGATGAGC 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetProAspAla-----LysLysGlnGlyArgSerAsnLysAlaMetThrPhePhe 17
                                                                                                                                                                                                                                                                                             PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR, TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transport; Sugar transport; Transmembrane; Symport;
Complete protecome.
SIMILARITY: Belongs to the sugar transporter family.
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07E08935ED8E3F8E CRC64;
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9 (POTENTIAL).
PERIPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
PERIPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                             EMBL; U28377; AAA69110.1; -...
EMBL; AE016376; AAA75980.1; -...
PRR; F65079; F65079.
ECCGGDE; EG12148; GalP.
INTERPRO; IPRO07114; MFS.
INTERPRO; IPRO07114; MFS.
INTERPRO; IPRO05829; Sug_transporter.
INTERPRO; IPRO05829; Sug_transporter.
INTERPRO; IPRO05829; Sug_transporter.
INTERPRO; IPRO05829; Sug_transporter.
INTERPRO; IPRO0363; Sugar_transpt.
PRO0883; Sugar_transpt.
PRO0883; Sugar_transpt.
PRINTS; PRO0111; SUGRITNSFORT.
TICRFAMS; TIGRO0879; SP; 1.
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SOLITE TETET TETET

1124 1298 1004 1064 1184 347 367 195 ProArgiripheAlaAlaLysArgArgPheValAspAlaGluArgValLeuLeuArgieu 214 824 234 884 944 327 GCCGTGGGCTACGCGCTCATGATCGCGCCGGTGTACACCGGCGAGGTGTCGCCGGCGTCG 524 137 584 644 174 704 194 764 ATGGGCATACTGAACCTCTACTCGCTCATCGGCTCCTTCGCGGCGGGGGGGACGTCGGAC 344 464 LysLeudlyArgLysLysSerLeumetIleGlyAlaIleLeuPheValAlaGlySerLeu 97 57 1125 GGGCGGCGGCGCTGTTGCTGGCAGCACGGGGGGGATAATCCTCTCCCTCATCGGCCTC |||::|||:::|||TyrLeuSerAspThrAlaPheSer-----TyrThrGlyAlaTrpArgTrpMetLeu CCGCGGTGGCTGGTCATGAAGGGACGCCTCGCGGACGCCCAAGGTGGTGCTGGAAGACGCC 765 TCCGACACGGCGGAGGAGGCCGCGTGGCCGACATCAAGGCCGCCGCCGCCATC |||||||::: ||||||| :::||||::: ::: 215 ArgAspThrSerAlaGluAlaLysArgGluLeuAspGluIleArgGluSerLeuGlnVal 825 CCTGAGGAGCTCGACGGCGACGTGGTGACCGTCCCCAAGAGAGGGAGCGGAAACGAGAAG 885 CGGGTGTGGAAGGAGCTCATCCTGTCCCCGACCCCGGCCATGCGGCGCATCCTGCTGTCC ...--Trp-----AlaLeuPheLysGluAsnSerAsnPheArgArgAlaValPheLeu GGGATCGGCATCCACTTCTTCCAGCATGCGTTGGGCATTCACTCCGTCGTCTTCTACAGC |||::: ::: :::|||::: 255 GlyValLeuLeuGlnValMetGlnGlnPheThrGlyMetAsnVallleMetTyrTyrAla 1005 CCTCTCGTGTTCAAGAGCCCCGGATTAACGAACGACAAACACTTCTTGGGCACCACTTGG ||| :::|||::: |ProLysilePheGluLeuAlaGlyTyrThrAsnThrThrGluGlnMetTrpGlyThrVal CCGTTCGGTGTCACCAAGAGGCTTTTCATCTTGTTGGCGACTTTCTTCATCGACGGCGTC 295 IleValGlyLeuThrAsnValLeuAlaThrPheIleAlaIleGlyLeuValAspArgTrp |||||||::: |||:::||| 328 AlaAlaGlyMetGlyValLeuGlyThrMetMetHisIleGlyIleHisSerProSerAla 348 GlnTyrPheAlaileAlaMetLeuLeuMetPheIleValGlyPheAlaMetSerAlaGly GCGCGTGGCTTCCTGACGTCGTTCCCGGAGGTGTTCATCAACTTCGGCATCCTGCTCGGG TACGTCTCGAACTATGCTTTCTCCCGCTTGCCGCTGAACCTCGGGTGGCGCATCATGCTC .----ThrieuGlyPheLeuValMet 1185 GGCGCCGGGCTCACCGTCGGC-----CAGCACCCCGACGCCAAGATACCTTGGGCC 1239 ATCGGCCTAAGCATCGCCTCCACCCTCGCCTACGTCGCCTTCTTCTCCATCGGCCTTGGGC CTCATGGGGTTCGCCGTCAACTACGCCATGCTCATGTTCGGCCGCCTTCGTGGCCGGCATC ---SerGly 315 GlyArgLysProThrLeu-

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                                                                                                                                         1419 CTGTCCAAGGCCATCACCATCGGCGGCAGCTTCTTCCTCTACTCCGGCATCGCCGCGCTC 1478
                                                                                                                                                                                                                                       GCCTGGGTGTTCTTCTACACCTACCTCCCGGAGACCCGGGCCGGACGACGTGGAGGAGATG 1538
                                                                              ::: ||| |||||||::: 388 Thr SerThr Asn Trylle Ala Asn Metile Val Gly Ala Thr Phe Leuthr 407
ProLeuIleTrpValLeuCysSerGluIleGlnProLeuLysGlyArgAspPheGlyIle 387
                                                                                                                                                                                                                                                                                            447
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                                           TCGCTCGGCGTCGCCGAACGCGCTCACCAGCGGCGTCATCTCCATGACCTTCCTGTCG
                                                                                                                                                                                       408 MetLeuAsnThrLeuGlyAsnAlaAsnThrPheTrpValTyrAlaAlaLeuAsnValLeu
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MIDLINES-86076631; PubMed=7502582;
Vandenbol M., Durand P., Portetelle D., Hilger F.;
Vandenbol M., Durand P., Portetelle D., Hilger F.;
"Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the Tyl-H3 retrotransposon, the sufil(+) frameshift suppressor gene for tNNA-Gly, the yeast transfer NNA-Thr-la and a delta element.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myo-inositol transporter 2.

ITR2 OR YOL103W OR HRB612.
Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
MEDLINE=91250431; PubMed=2040626;
Michawa J.-I., Tsukagoshi Y., Yamashita S.;
"Isolation and characterization of two distinct myo-inositol transporter genes of Saccharomyces cerevisiae.";
J. Biol. Chem. 266:11184-11191(1991).
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EMBL; Z48149; CAA88159.1; -.
EMBL; Z4845, CAA98119.1; -.
EMBL; Z4845, CAA98119.1; -.
EMBL; Z48453.8
GermOnline; 143525; -.
SGD; S0005463; IRR2-
GO; GO:000536; F: RP2-
HOSTOR TRANSPORTER activity; IMP.
GO; GO:0015798; P: RP2-
HOSTOR TRANSPORT; IMP.
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-!- FUNCTION: MINOR TRANSPORTER FOR MYO-INOSITOL.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the sugar transporter family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612 AA.
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InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
Pfam; PF00083; Sugar_tr; 1.
PRINTS; PR00171; SUGRIRNSPORT.
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28-FEB-2003
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GAGGCCGTCGCGCCGAAGAAGAAGGGCCAACGTCCGGTTCGCCTTCGCCTGCGCCATCCTC 176
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ValGlylleGlySerLeuileSerProLeuPheileSerGluileAlaProLysMetile 238
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|AlaSerIleSerGlyPheMetPheGlyTyrAspThrGlyTyrIleSerSerAlaLeuIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 ATGGGGTTCGCCGTCAACTACGCCATGCTCATGTTCGGCCGCTTCGTGGCCGGCATCGGC
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
4 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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48E733102BAD7298 CRC64;
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Matches:
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ID YFIG BACSU
AC P54723;
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01-OCT-1996
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239 ArgGlyArgLeuThrVallleAsnSerLeuTrpLeuThrGlyGlyGlnLeuIleAlaTyr 258
                         647
                                                                                                                      CGGTGGTGGTCATGAAGGGACGCCTCGCGACGCCAAGGTGGTGCTGGAGAAGACCTCC 767
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PheSerGlyThrIlePheGluThrValGlyPheLysAsnSerSer-----AlaVal
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| SerllelleValSerGlyThrAsnPheValPheThrLeulleAlaPheCysIleAsp
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                                      ATCGGCGCGCCGCCGTCCGTGCTCGCGCTCATGGTGCTCGGCATGCCGGAGTCGCCG
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                        GTCTCGAACTATGCTTTCTCCCGCTTGCCGCTGAACCTCGGGTGGCGCATCATGCTCGGC
                                                                                                                                                                                             317 ValAsnThrGlu------AspGluIleIleAspGlnLysVal------
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KURDINE-98044031; PubMedge 334337;

RA Agevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Agevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Agevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Haga K., Haich W.F., Itaya M., Jones L.,

RA Guiseppi G., Guy B.J., Haga K., Haich W.F., Itaya M., Jones L.,

RA Guiseppi G., Guy B.J., Haga K., Haich J., Harwood C.R., Henaut A.,

RA Guiseppi G., Guy B.J., Rashara Y., Klaerr-Banchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kamano M.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kamano M.,

RA Medina N., Mellado R.P., Mizuno M., Mosell D., Dazarevic V.,

RA Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,

RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadaie Y.,

RA Settyuchi J., Sekwaka A., Seiro S., Schroeter R., Scoffene F.,

RA Sorckin A., Taconi E., Takahashi H., Takemaru K.,

RA Tosato V., Uchiyama S., Vandenbol M., Wannier F., Vassarotti A.,

RA Viari A., Wambut R., Wedler E., Wedler H., Wanner E., Vashida K., Yoshikawa H.F., Zumstein E., Woohlikawa H.F., Zongtein E., Woohlikawa H.F., Zongtein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto H., Uchiyama S., Fajar A.N., Ogasawara N., Sekiguchi J.; "Determination of a 12 kb nucleotide sequence around the 76 degrees region of the Bacillus subtilis chromosome."; Microbiology 142:1417-1421(1596).
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--- SUBCELLUIAR (CONTION): Integral membrane protein (Probable).
--- SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                   Hypothetical metabolite transport protein yfig. YFIG OR BSU08260.
                                                                                                                                           Last sequence update)
Last annotation update)
482 AA.
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SubtiList; BG11854; YfiG.
InterPro; IPRO0114; MFG.
InterPro; IPR005828; Sub_transporter.
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     STANDARD;
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CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
6 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
8 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                        Transmembrane;
                                                                                              FALSE NEG
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                                                PRINTS; FKUCALL,
TIGREAMS; TROUGHOSTS; 1.
PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR TRANSPORT 1; FALSE
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
Hypothetical protein; Transport; Transmemt
Prochetical protein; Transport; Transmemt
Officers of the comment o
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                    (POTENTIAL)
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InterPro, IPR005829; Sug_transporter.
InterPro; IPR00363; Sugar transpt.
Pfam, PF00083; Sugar tr, 1
PRINTS; PR00171; SUGRIRNSPORT.
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555.50
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Best Local Similarity:
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PheThrPheProlleLeuLeuAsnHislleGlyMetSerAlaThrPhePheIlePheVal 434
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                                                                                                                                                        LeuArgValLeuArgGln1leArgGluAspSer---GlnAlaGlnGlnGlu1leLysGlu
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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813AFC8AFA7AA583 CRC64;
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DOMAIN 1 23 CYTOPLASHIC (POTENTIAL).

TANNOMEN 24 44 (POTENTIAL).
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PROSITE; PSCO850; NFS; 1.
PROSITE; PSCO216; SUGAR_TRANSPORT_1; 1.
PROSITE; PSCO217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                              InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
InterPro; IPR003663; Sugar_transpt.
PR000033; Sugar_tri.
PRINTS; PR00171; SUGRTRNSPORT.
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                                                                                                        EMBL; AC007259; AAD49995.1; -. EMBL; AY059781; AAL24129.1; -. EMBL; AY054249; AAL06908.1; -.
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                                                                                   EMBL; X55350; CAA39037.1; -.
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PIR; S12042; S12042.
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522 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. Columbia;

X MEDLINE=21016719; PubMed=11130712;
Theologis A., Beker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Theologis A., Beker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buchler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,
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Durn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
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A Durn P., E. Goldmaith A.D., Haas B., Hancen N.F., Hughes B., Huizar L.,
A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Lin S.X., Liu Z.A., Lurco J.S., Maiti R., Marziali A.,
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Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
Sequence and analysis of chromosome l of the plant Arabidopsis
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C STRAIN—CV. Columbia;

MEDLINE=2295485C; PubMed=14593172;

MEDLINE=2295485C; PubMed=14593172;

MEDLINE=2295485C; PubMed=14593172;

A yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Cheuk R.F.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Tange C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

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A rakawa T., Banh J., Banno F., Bowser L., Brocks S.Y., Carninci P.,

A rakawa T., Dohnson-Hopson C., Hsuan V.W., Ilda K., Karnes N.,

A kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids,
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
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STRAINsev. Landaberg erecta;
STRAINsev. Landaberg Expension of Strain of Strain of Strain of Strain of Strain of Structure, genomic organization and heterologous expression of a glucose transporter from Arabidopsis thaliana.";
EMBO J. 9:1045-3050(1990).
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                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) 19-Cose transporter (Sugar carrier) STP1 OR ATIG11260 OR 128P6.9
                                               522 AA.
                                                                 P23586; Q9SXB1;
01-NOV-1991 (Rel. 20, Created)
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Science 302:842-846(2003)
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                                               STANDARD;
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92 GGAGATGGCTTCCGCCGCGCTGCCGGAGGACGCCGAAGAAGAAGGGCCAACGTCCG 151
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                                                                                                                41 edlylleserGlydlyvalThrSerMetProSerPheLeuLysArgPhePheProSerVa
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61 lTyrargLysGlnGlnGlnGluAspAlaSerThrAsnGlnTyrCysGlnTyrAspSerProTh
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                                                                                   152 GTTCGCCTTCGCCTGCGCCATCCTCGCCTCCATGACCTCCATCCTCCTCGGCTACGATAT
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                                                           CGTGGCCGGCATCGCCGTGGGCTACGCGCTCATGATCGCGCCGGTGTACACCGCCGAGGT 511
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yileLeuValAlaGluValLeuAsnTyrPhePheAlaLysIleLysGlyGlyTrpGlyTr 201
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eMetPheTyrAlaProValLeuPheAsnThrIleGlyPheThrThrAspAlaSerLeuMe 322
sAlaGlyAlaLeuIleAsnGlyPheAlaLysHisValTrpMetLeuIleValGlyArgIl 141
                                                                                                                                                                                                                                                                                                                                                                                              GCGCATCATGCTCGGCATCGGCGCGCGCGTCCGTGCTGCTCGCGCCTCATGGTGCTCGG 691
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eProLeuGlulleArgSerAlaAlaGlnSerIleThrValSerValAsnMetIlePheTh 437
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pArgLeuSerLeuGlyGlyAlaValValProAlaLeuIleIleThrIleGlySerLeuVa
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rValAlaGlyPheAlaTrpSerTrpGlyProLeuGlyTrpLeuValProSerGluIlePh
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                                                                                                                                                    Chlorella kessleri.
Bukaryota; Viridiplantae, Chlorophyta; Trebouxiophyceae, Chlorellales,
Chlorellales incertae sedis; Parachlorella.
NCBI_TaxID=3074;
                                                                                                                                                                                                                                    Stadler R., Wolf K., Hilgarth C., Tanner W., Sauer N.K., "Subcellular localization of the inducible Chlorella HUP1 monosaccharide-H+ symporter and cloning of a Co-induced galactose-H+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugar transport; Symport; Repeat;
                                                                                                                                                                                                                                                                                 plant Physiol. 107:33-41(1995).
-- FUNCTION: Active uptake of hexoses.
-- SUBCELLUAR LOCATION: Integral membrane protein.
-- SUBILARITY: Belongs to the sugar transporter family.
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CYTOPELAGIC (POTENTIAL).
3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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             UThrLysGlyIleProlleGluGluMetGlyGlnValTrp
                                                                                                        Last sequence update)
Last annotation update)
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InterPro; IPR005829; Sub transporter.
InterPro; IPR005829; Sugar transpt.
InterPro; IPR003663; Sugar transpt.
PRIMTS; PR00111; SUGRTRNSPORT.
IGRPAMS; TIGR00879; SP; 1.
PR051TE; PS50850; MRS; 1.
PR051TE; PS00211; SUGAR TRANSPORT.
ITARSmembrane; Transport; Sugar transport;
Multigene family.

20 CYTOPLASMIC ()
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                                                                                            Created)
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15-JUL-1998 (Rel. 36,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=95175627;
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                                                                                                              1035 AACGACAAAACACTTCTTGGGCACCACTTGGCCGTTCGGTGTCACCAAGAGGCTTTTCATC 1094
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||| ThracgargTyrMetProGlnLeuLeuThrSerPheVallleGlnPhePheGlnBhe 300
                                                                                                                                            SerSerAlaAlaLeuLeuAsnThrVal---ValValGlyAlaValAsnValGlySerThr 339
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|GlyGlnTyrGlyThrGluAspLeuPrOHisProValSerAlaGlyValLeuAlaValIle 397
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Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellales incertae sedis; Parachlorella.
NCBI_TaxID=3074;
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CysllePhelleAlaGlyPheAlaTrpSerTrpGlyProMetGlyTrpLeUroSer
                                                   975 TTGGGCATTCACTCCGTCGTCTTCTACAGCCCTCTCGTGTTCAAGAGCCCCCGGATTAACG
                                                                      |||||||::::::::::::||||||| |||::::::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ThrGlyIleaBhalaileileIlePheTyrvalProValLeuBheSerSerLeuGlySerAla
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MEDLINE=91330335; PubMed=1868571;

MO1f K., Tanner W., Sauer N.;

"The Chlorella H+/haxose cotransporter gene.";

Curr. Genet. 19:215-219(1991).

-!- FUNCTION: Active uptake of hexoses.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- INDUCTION: By glucose.

-!- SIMILARITY: Belongs to the sugar transporter family.
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MEDLINE=90092538; PubMed=2599110;
Sauer N., Tanner W.; from Chlorella. cDNA cloning
"The hexose carrier from Chlorella. cDNA cloning
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Last annotation update)
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P1566; 039523;
01-APK-1990 (Rel. 14, Created)
15-JUL-1998 (Rel. 36, Last seq
28-FEB-2003 (Rel. 41, Last ann
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HUP1.
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Mismatches:
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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|AlaPheMetAlaAlaCysGlyGlyGlyLeuLeuClyTyrAspAsnGlyValThrClyGly
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PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transmembrane; Transport; Sugar transport; Symport; Repeat;
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EXTRACELULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

MISSING (IN REF. 1).

P. - L (IN REF. 1).
C - R (IN REF. 1).
C - R (IN REF. 1).
W, 3B238E8710AA2237 CRC64;
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2 (POTENTIAL),
CYTOPLASMIC (POTENTIAL).
3 (POTENTIAL).
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                                                                                            EMBL, X55349; CAA39036.1; -.
PTR, S14144; S14144.
InterPro; IPR007114; MFS.
InterPro; IPR005829; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR00363; Sugar_transpt.
Pfam; PF00081; Sugar_transpt.
Pfam; PF00081; Sugar_transpt.
TIGRFAMS; TIGR00879; SP; 1.
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Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Suguitra M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: Belongs to the sugar transporter family.
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Bacteria, Cyanobacteria, Chroococcales; Synechocystis.
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GTR OR GLCP OR SLL0771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 CTCGCCTCCATGACCTCCATCCTCCGCTACGATATCGGGGTGATGAGCGGGCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 AlaAlaLeuGlnLysHisPheGlnThrAspSerLeuLeuThrGlyLeuSerValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AlaLeuLeuGlySerAlaLeuGlyAlaPheGlyAlaGlyProIleAlaAspArgHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 CTGTACATCAAGAAGGACTTCAACATCAGTGACGGAAGGTGGAGGTTCTCATGGGCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 CGGCGGTACACCATCGTGTTCGCCGCCGTCATATTCTTCGCGGGGGSGTTCCTCATGGGG
                                                                                                                                                                                               FIGHTANS; 110. PROSTE; PSS0155; 1. PROSTE; PSS0156; SUGAR TRANSPORT 1; 1. PROSTIE; PS00217; SUGAR TRANSPORT 2; 1. PROSTIE; PS00217; SUGAR TRANSPORT 2; 1. Transmembrane; Transport; Sugar Lransport; Complete proteome. Transmembrane; Transmembrane; CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                            1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                              3 (POTENTIAL). EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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D7EC545C4FB38D22 CRC64;
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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EMBL; X16472; CAA34492.1; -.
EMBL; D64000; BAA10117.1; -.
PIF; S10014; S10014.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005828; Sug_transporter.
InterPro; IPR005829; Sugar_transpt.
Pfam; PF00083; Sugar_tr.; I.
PRINTS; PR00171; SUGRIRNSPORT.
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| 6 2 2 3 3 5 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 9 2 8 6 | -:: LeuLeuSerArgArgGlyGly 262 TCTTCCAGCATGGGCATT 983 | 321 115 115 341 120 358 376 | CHTCACGTGGGTGTACAGCTCG 1322 |
|--|------------------|--|---|---|
| 4 TTCCTCGCTCAACTACGCCATGCTCGGCCGCTTCGTGCCGGCATCGCCGTGGCC 3 LeuProPheThrIleTrpAspPhellePheTrpArgValleuGlyGlyIleGlyValGly 4 TACGCGCTCATGATCGCCGCGTGTACACCGCCGGGGTGCGCGTGGCGTGGCGTGGCTGGC | | Pheserasp | | 3 CTGGCCTACGTGGCCTTCTTCTCCATGGGCCCTGTGACGTGGACGTCGACGCGCAACGGGGATGATGASALySIL6ArgAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaA |
| 4 1 4 1 8 1 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 2 8 2 8 2 4 8 | 2 9 2 9 2 9 2 | 104, 30, 115, 115, 120, 120, | 126 13 3 3 3 4 4 1 1 4 4 1 1 4 4 1 1 4 1 1 4 1 1 4 1 1 4 1 1 4 1 1 4 1 |
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Search completed: June 30, 2004, 18:44:40 Job time: 71.5 secs

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Q844m3 prunus cera
Q91592 arabidopsis
Q1592 arabidopsis
Q15302 arabidopsis
Q15075 beta vulgar
Q84xi7 prunus domes
P93075 beta vulgar
P93075 beta vulgar
Q8xih6 arabidopsis
Q8xih7 arabidopsis
Q8xih6 arabidopsis
Q8xin2 aplum grave
Q7xb36 arabidopsis
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Q9xv10 oryza sativ
Q81xv10 lea europa
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Oryza sativa (Rice)

Oryza sativa (Rice)

Sukaryota, Viridiplantae Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ©945B5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Q9C757
Q7XRI6
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Q83EH4
Q34718
Q93WT7
                        Q84QH3
Q9LS92
Q7XA50
Q84XI7
Q84XI1
P93076
P93075
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Q84RI2
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Q7XB36
Q8RVQ2
Q9RNS0
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09AUM9
08W2W8
07XFD6
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09SKT9
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-MODEL=frame+.n2p.mcdel-bEv=xlp
-MODEL=frame+.n2p.mcdel-bEv=xlp
-MODEL=frame+.n2p.mcdel-bEv=xlp
-De_CGDZ_1/USF7O_Spool_p/US1005190/runat_30062004_164723_20411/app_query.fasta_1.2183
-DB=SPTREMBL_25.-QFMT=fastan -SUFFIX.rspt.-MINMATCH=0.1_LOOPCL=0.-LOOPEXT=0
-UNITS=blts.-START=1.END=-1.MATRXT=blosum62.-TRANS=human40.cdi.-LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0.ALIGN=15.MODE=LOCAL
-OUTPWT=ptc -NORM=ext -HEAPSIZE=500 -MINIEN=0.-MAXIEN=200000000
-USRE-STOOLOGO -NORM=ext -HEAPSIZE=500 -MINIEN=0.ALIGN=1200000000
-USRE-STOOLOGO -NAGG_SCORES=0.MATT -DSPBLOOCK=170 -LONGIGG
-NO_MMAP -LARGEQUERY -NEG_SCORES=0.FMATT -DSPBLOOCK=170 -LONGIGG
-DST_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS 1.*XGAPOP=10 -XGAPBEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                     Description
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                  protein search, using frame_plus_n2p model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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AsnGluLysArgValTrpLysGluLeulleLeuSerProThrProAlaMetArgArglle 347
CTCGCCTGGGTGTTCTTCTACACCTACCTCCCGGAACCCGGGGCCGGACGCTGGAGGAG
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Q8LHC3;
Q1-CCT-2002 (TERMBLrel. 22, Created)
01-CCT-2002 (TERMBLrel. 22, Last sequence update)
01-CCT-2003 (TERMBLrel. 25, Last annotation update)
01-CCT-2003 (TERMBLrel. 25, Last sequence update)
0-CCT-2003 (TERMBLrel. 26, Last sequence u
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       GO; GO:0008643; P:carbohydrate transport; IEA.
InterPro; IPR007114; MFS.
InterPro; IPR007114; MFS.
InterPro; IPR007863; Sugar_transporter.
InterPro; IPR00829; Sugar_transporter.
InterPro; IPR00829; Sugar_transporter.
Ffam; PP00083; Sugar_tr; 1.
Ffam; PP00083; Sugar_tr; 1.
FFAM; PP00171; SUGRIRNSPORT.
ITGRRAMA; TIGR00879; SP; 1.
FROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
FROSITE; PS00216; SUGAR_TRANSPORT_2; 1.
Sugar_transport; Transmembrane; Transport.
SEQUENCE 577 AA; 61178 MW; 95651621AE980CD4 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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01-UDN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative sorbitol transporter.
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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

STAIN=cv. Nipporbare;

A Sasaki T., Matsumoto T., Yamamoto K.;

"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone: Pot/SBEBS.";

I Submitted (NOV-201) to the EMBI/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIM)

C -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIM)

C -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIM)

R GAMEN; ABOOM 20215; F: SUBGAR PORTER TRANSPORTER FAMILY.

R GO: GO: 0005321; F: Sugar porter activity; IEA.

GO: GO: 0005321; F: Exansporter activity; IEA.

R GO: GO: 0005321; F: Exansporter activity; IEA.

R GO: GO: 0005321; F: Exansporter activity; IEA.

R INTERPRO; IPRO0828; SUB_transporter.

InterPro; IPRO0828; SUB_transporter.

InterPro; IPRO08828; SUB_transporter.

INTERPRO; INTERPROSP29; SUB_TRANSPORT.

R INTERPRO; INTERPROSP29; SUB_TRANSPORT.

R INTERPRO; INTERPROSP29; SEQ. TANSPORTER.

R INTERPRO; INTERPROSP39; SUB_TRANSPORT.

R INTERPRO; INTERPROSP39; SED. 1.

R PRINTS; PRO0171; SUGRIRNSPORT.
                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2.
SUGAR_transport; Transmembrane; Transport.
SEQUENCE 511 AA; 54606 MW; ECF9573E22B3C625 CRC64;
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|IeAspAlaValValLeuTyrSerProArg1lePheGluLysAlaGlyIleThrAsnPro
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                         Prunus cerasus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                           STRAIN=cv. Montmorency; TISSUE=Fruit;
MEDLINE=22578818; PubMed=12692316;
Gao Z., Maurousset L., Lemoine R., Yoo S.D., Van Nocker S.,
Loescher W.; rexpression, and Characterization of Sorbitol Transporters
from Developing Sour Cherry Fruit and Leaf Sink Tissues:";
Plant Physiol. 131:1566-1575(2003).
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SEQUENCE FROM N.A.
SUITABLEACY, MOINTENERS DEFRUIT,
Zhifang G., Loescher W.H.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY10658, AAM44082.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005551; F:transporter activity; IEA.
GO; GO:0005551; F:transporter activity; IEA.
GO; GO:0006643; F:transporter activity; IEA.
GO; GO:0006643; F:transporter activity; IEA.
InterPro; IPR007828; Sub_transporter.
InterPro; IPR008629; Sub_transporter.
InterPro; IPR008629; Sug_transporter.
Ffam; PF00083; sugar_transporter.
Ffam; PF00083; sugar_tri.1;
FRINTS; PR00171; SUGRTRNSPORT.
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PROSITE; PS00216; SUGAR TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
SEQUENCE 5.38 AA; 58569 MW; ADDD03B983C6D358 CRC64;
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Best Local Similarity:
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SEQUENCE FROM N.A.
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1581 GAGCCAGCCAAGGAGAAGAAGAAGGTGGAAATGGCCGCCACTAACTGATCAAACTAACCG 1640
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                 CCAGAGCGAGCCTCCTCCTCTGCACCACCGGAGATGGCTTCCGCCGCGCTGCCGGAG
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| ProGluAsnArgThrAlaProSerProProPro-----ValLysHisValProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugar transporter protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                          s:
                                                                                                                                                                                                                                                                                                                       Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA RES. 7:131-135 (2000).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY STANDIARLY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

EMBL, AB026654; BAB01812.1, -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:000531; F:sugar porter activity; IEA.

GO; GO:0005315; F:transporter activity; IEA.

GO; GO:0008643; P:carbohydrate transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50850; MPS; 1.
PROSITE; PS00216; SUGAR TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT 2: 1.
SUGAR transport; Transmembrane; Transport.
SEQUENCE 539 AA; 58102 MW; 36B389284E5563A0 CRC64;
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328
69
116
11
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
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Gaps:
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Interpro; IPR005828; Sub transporter.
Interpro; IPR005829; Sugar_transporter.
Interpro; IPR005829; Sugar_transporter.
Pfain; PF00083; sugar_tr; 1.
PRINTS; PR00111; SUGRTRNSPORT.
IIGRPAMS; TIGR00879; SP; 1.
                                                                                                                                    PRT;
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75.76%
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| 52 MetSerGlyAlaAlaIleTyrIleLysArgAspLeuLysValSerAspGluGlnIleGlu 71 279 GTTCTCATGGGCATACTGACCTCATCGGTCCTTCGCGGGGGGGG | | GAGAGGGGGTGGAGGGGCTGTCCCCGGCCATGCGGCGCATGCGGGGTTCGGGGGTGCGGGTTCGTGGGGGGTTCGTGGGGGTTCGTGTCCCGGCCATGCGGGGGTTCGTGGGGGTTCGTGGGGGTTCGTGGGGTTCGGGGTTCGGGGTTCGGGGTTCGGGGTTCGGGGTTCGGGGATTCGTCTTCCGGGATGCGTTGGGGATTCACTCGTGTTTTC 99 | 1059 ACTIGGCCGTTCGCGAGGCCTTTCATCTTCTTGGCGACTTTCTCATCGAC 1118 330 ThrvalalavaldlyPhevalLysThrvalPhelleLeualaalaThrPheThrLeuasp 349 1119 GGCGTCGGCGGCGCGCTGTTGCTGGGCAGCAGGATATCCTCTCTCT |
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| Oy 1254 GCCTCCACCCTCGCCTACGTCGCCTTCTCCATCGCCCTTGGCCCCATCACGTGGTG 1313 400 AlaThrValMetThrTyrValAlaThrDheSerIleGlyAlaGlyProlle[| 1614 GCCGCACTAAC 1625 1614 GCCGCCACTAAC 1625 SULT 5 KA50 Q7XA50 PRELIMINARY; PRT; 523 AA. Q7XA50 Q7XA50 Q1-CCT-2003 (TrEMBLrel. 25, Last sequence update) 01-CCT-2003 (TrEMBLrel. 25, Last sequence max(soybean) Sorbitol-like transporter. STP. STP. Supply an analysis of tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Audicotyledons; core eudicots, rosids; | Tax I, Fadales; Fabaceae; Fapilionolueae; Finance TaxID=3847; NCE FROM N.A. NCE Williams; N. Aivalakis G., Katinakis P.; N. Aivalakis G., Katinakis P.; on metabolism in developing roots and lateral rann metabolism in developing roots and lateral rannsporter."; trem as seedlings. Expression of GmSTP gene codition for the EMBL/GenBank/DDBJ databa AJS63337; CAD91337.1; AJS63367; CAD91337.1; NCE 523 AA; 56489 MW; 3A586397262F1C4B CRC6 | Alignment Scores: Pred. No.: 1.61e-86 |

| Best Local Similarity: 67.30\$ Mismatches: 98 Query Match: 10 14.47\$ Indels: 3 DB: 10 15.20.17) X 084KI7 (1-50.9) AGAGAGAGGCAACGTCCGGTTCGCCTTCGCCTCCTCGCCTCCATGACCTCC AGAGAGAGGCAACGTCCGGTTCGCCTTCGCCTCCTCGCCTCCATGACCTCC AGAGAGAGGCAACGTCCGGTTCGCTTCGCCTCCTCCTCCTCCTCCTCCTCCT | 432 ATCCTANTATCOCCACCTCOTCCCCCCCCCCCCCCCCCCC | y 1092 ATCTIGITGGCGACTTICTICACGGCGGCGGCGGCGGCCGCTGTTGCTGGGCAGC 1151 ::: |
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| 98 99 99 99 99 99 99 99 99 99 99 99 99 9 | 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 | Qy |
| Qy 1359 TCGCTCGCCCCAACCGCGTCACCAGCGCGTCATCTCCTGTCG 1418 429 AlaalaGlyValAlaValAsTAPTDTTTTTCTTCTCTTCTTCTTCTGCCGCGTTC 1478 429 AlaalaGlyValAlaValAsTAPTDTTTTCTTCTTCTTCTTCTTCTTCTCGCCGTTC 1478 429 LuttrargalaInTTTTTGCGCGCGCGGCTTCTTCTTCTTCTTCTCGCCGTTC 1478 429 LeuthrargalaInTTTTTGGCGCGCGGCTTCTTCTTCTTCTGGCGGTTCTTTT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | REBULT 6 094KI7 AC 084KI7 AC 084KI7 O1-JUN-2003 (TrEMBLrel. 24, Created) DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) DT 01-JUN-2003 (TrEMBLrel. 25, Last annotation update) DT 01-JUN-2003 (TrEMBLrel. 25, Last annotation update) DT 01-JUN-2003 (TrEMBLrel. 25, Last sequence update) DT 01-JUN-2003 (TrEMBLrel. 26, Last sequence update) DT 01-JUN-2003 (TrEMBLrel. 27, Last sequence update) DT 01-JUN-2003 (TrEMBLrel. 27, Last sequence update) Corcarasis Tremsporter. Corcarasis Tremsporter. Corcarasis Tremsporter. Corcarasis Tremsporter. Corcarasis Tremsporter. RA MEDINE-225/8918; PubMed=12692316; RA MEDINE-225/8918; PubMed=12693316; RA MEDINE-225/891 | Alignment Scores: Pred. No.: Score: Score: 1607.00 Matches: 319 Percent Similarity: 78.48% Conservative: 53 |

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GTCGGCCAGCACCCCGACGCCAAGATACCTTGGCCCATCGGCCTAAGCATCGCCTCCACC 1262
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                                                               1 MetThrSerIleLeuLeuGlyTyrAspIleGlyValMetSerGlyAlaSerLeuPheIle
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                                                                                                                                                   61 ThrileValLeuAlaGlyThrilePhePheIleGlyAlaLeuLeuMetGlyPheAlaPro
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  US-10-051-902A-21 (1-2017) x Q84RI1 (1-481)
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=cv. Mutan; TISSUE=Fruit;

Zhidang G., Jayanty S., Beadun of apple fruit sorbitol transporter.";

L. Cloning and characterization of apple fruit sorbitol transporter.";

EMBL, AY213401, AA089955.1;

R. GO; GO:0016020; C:membrane; IEA.

R. GO; GO:000521; F:sugar porter activity; IEA.

R. GO; GO:0005251; F:sugar porter activity; IEA.

R. InterPro; IPR007114; MFS.

R. InterPro; IPR005628; Sugar transporter.

R. InterPro; IPR005829; Sug_transporter.

R. InterPro; IPR005829; Sug_transporter.
                      ValAlaGlyMetIleAlaSerLeuLeuCysLeuGlyThrSerLeuThrIleVal---Asp
                                                                                                            PheLeuTyrAlaGly1leAlaThrValGlyTrpValPhePheTyrThrMetLeuProGlu
                                                                                   CACCCCGACGCCAAGATACCTTGGGCCATCGGCCTAAGCATCGCCTCCACCCTCGCCTAC
                                                                                                                                                                     GTCGCCTTCTTCTCCATCGGCCTTGGCCCCATCACGTGGGTGTACAGCTCGGAGATCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorbitol transporter.
SOT2.
Malus domestica (Apple) (Malus sylvestris).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Rosales, Rosaceae, Maloideae, Malus.
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ThrGlnGlyArgThrLeuGluAspMetGluValLeuPheGly 489
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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PROSTIE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSTIE; PS00217; SUGAR_TRANSPORT_2; 1.
SEQUENCE 481 AA; 52566 MW; A3C20EES
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InterPro; IPR00563; Sub_transporter.
InterPro; IPR00563; Sugar_transpt.
InterPro; IPR005829; Sug_transporter.
Pfam, PF00083; sugar_tr; I.
PRINTS; PR00171; SUGÄTRNSPORT.
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               PERM; PF00083; SUGAT LT; 1.
PRINTS; PR00111; SUGRTRNSPORT.
TIGRPAMS; TIGRO0879; SP; 1.
PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
SUGAR_TRANSPORT_2; 1.
SUGAR_TRANSPORT_5 1.
SUGAR_TRANSPORT_5 1.
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Mismatches:
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                     367 ThrSerValGlyGlyMetIleIleAlaIleLeuThrLeuAlaMetSerLeuThrValIle
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                                                                                                                     1206 GGCCAGCACCCCGACGCCAAGATACCTTGGGCCATCGGCCTAAGCATCGCCTCCACCTC
                                                                                                                                             ---AspHisSerHisHisLysIleThrTrpAlaIleAlaLeuCysIleThrMetValCys
                                                                                                                                                                              GCCTACGTCGCCTTCTTCTCCATCGGCCTTGGCCCCATCACGTGGGTGTACAGCTCGGAG
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                                                                                                                                                                                                                                                                                                             446 ValSerGlyValIleSerIlePhePheLeuProLeuSerHisLySIleThrThrGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                 transporters from sugar beet (Accession Nos. U64902 and U64903) (PGRS7-017).", Plant Physiol. 113:663-663(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
-- BENBL; U64902; AABR8028-1;
-- PIR; T14606; T14606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta vulgaris (Sugar beet).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta,
Euryophytales, Amaranthaceae, Beta.
Caryophylales, Amaranthaceae, Beta.
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                                                                                                                                                                                                                                                                                                                                                                                                               CCGGAGACCCGCGGCCGGACGCTGGAGGAGATGAGCAAGCTGTTCGGCGAC-
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 25, Last annotation update)
BVCDNA-205 protein.
BVCDNA-205.
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buelli C.R., Kerchum K.A., Lee J.J., Ronning C.M., Koon H., Moffat K.S., Cronin L.A., Shen M. Vankhen S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerrille C.R., Copenhaver G.P., Preuss D., Nierman M.C., White O., Eisen J.A., Salbberg S.L., Fraser C.M., Venter J.C., Mile O., Eisen J.A., Sequence and analysis of chromosome 2 of the plant Arabidopsis
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                                                                                                                                                                                                             SIMILARITY)
                                                                                                                                                                                           Laborated (MAR-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMI STANDS ADDISON THE SUGAR TRANSPORTER PAMILY.

-:- SIMILARITY: BELOGNGS TO THE SUGAR TRANSPORTER PAMILY.

R DIR; H84536; H84536.

R GO; GO:000512; H84536.

R GO; GO:0005215; Fitnegral to membrane; IEA.

R GO; GO:0005215; Fitnensporter activity; IEA.

R GO; GO:0005215; Fitnensporter activity; IEA.

R GO; GO:0005215; Fitnensporter activity; IEA.

R InterPro; IPR007114; MFS.

R InterPro; IPR007828; Sub_transporter.

R InterPro; IPR005829; Sug_transporter.

R InterPro; IPR005829; Sug_transporter.

R PROSTIE; PS00803; SUGAR_LY.

R PROSTIE; PS00804; PRF; I.

R PROSTIE; PS00805; MFS; I.
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E646A59316C6A54B CRC64;
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Matches:
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PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
Sugar transport; Transmembrane; Transpo
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1579.00
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                                                                                                                  thaliana.";
Nature 402:761-768(1999)
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STRAIN=cv. Columbia;
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Best Local Similarity:
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|GlylleThrAsnAlaArgLysGlnLeuLeuAlaThrValAlaValGlyValValLysThr
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Arzbidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryote, Viridiplantae, Streptophyta; Core eudicots; core eudicots; rosids;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
enrosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
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STRAIN=CV. Columbia;
MEDLINE=20033487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBCENLIVIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL: AC007134; AAD26955.1; --
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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PROSITE; PS00216; SUGAR TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
SUGAR TRANSPORT 2; 1.
SUGAR TRANSPORT 3; 1.
SUGAR TRANSPORT 3; 1.
SUGAR TRANSPORT 3; 1.
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IPR003663; Sugar_transpt.
IPR005829; Sug_transporter.
0083; sugar_tr; 1.
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PRINTS, PR00171, SUGRTRNSPORT.
TIGRFAMS; TIGR00879; SP; 1.
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STRAIN=cv. Columbia;
Lin X.;
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Best Local Similarity:
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Malus domestica (Apple) (Malus sylvestris),
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Core eudicots; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Rosales; Rosaceae; Maloideae; Malus.
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A Zhifang G., Jayanty S., Beaudry R.M., Loescher W.H.;

Zhifang G., Jayanty S., Beaudry R.M., Loescher W.H.;

Zhifang G., Jayanty S., Beaudry R.M., Loescher W.H.;

"Cloning and characterization of apple fruit sorbitol trans;

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:000512; P:Sugar Dorter activity; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0005215; F:transporter activity; IEA.

R GO; GO:0005215; F:transporter activity; IEA.

R InterPro; IPR00563; Sugar Lansport; IEA.

R InterPro; IPR005639; Sugar transport.

R Pfam; PF00083; Sugar transporter.

R Pfam; PF00083; Sugar transporter.

R TIGRRAM; TIGR00879; Sugar transporter.

R PROSITE; PS00217; SUGAR TRANSPORT.1; 1.

R PROSITE; PS00216; SUGAR TRANSPORT.2; 1.

R PROSITE; PS00217; SUGAR TRANSPORT.2; 1.
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RN 113

RP SEQUENCE FROM N.A.

RC TISSUE=Phloem;

RX MEDINE=Z119681; PubMed=11251106;

RA Noiraud N., Maurousset L., Lemoine R.;

RA Noiraud N., Maurousset L., Lemoine R.;

RI "Identification of a mannitol transporter, agmatl, in celery phloem.";

RI "Identification of a mannitol transporter, agmatl, in celery phloem.";

RI "Identification of a mannitol transporter, agmatl, in celery phloem.";

RI "Identification of a mannitol transporter, provided and to the phloem.";

RI "Identification of a mannitol transporter FAMILY.

CC --- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

CC --- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

CC --- SIMILARITY: BELONGS TO THE GARD TRANSPORTER FAMILY.

DR GO; GO:0005311; F: transporter activity; IEA.

DR GO; GO:000515; F: transporter activity; IEA.

DR GO; GO:000543; F: transporter.

DR InterPro; IPRO05828; Sub_transporter.

DR InterPro; IPRO05828; Sub_transporter.

DR InterPro; IPRO05829; Sug_transporter.

DR InterPro; IPRO05829; Sug_transporter.

DR PRINTS; PRO171; SUGRTRNSPORT.

DR TIRRAMS; TIRRAMS, TIRRAMSPORT.

DR TIRRAMS; TIRRAMS, TIRRAMSPORT.

DR TIRRAMS, TIRRAMS, TIRRAMSPORT.
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                                                                                                                               GlullePheProLeuArgLeuArgAlaGlnGlyCysGlyMetGlyValAlaValAsnArg
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots; asteri
campanulids, Apiales, Apiaceae, Apioideae, apioid superclade,
Apium clade, Apium.
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TIGROUB/>, T.
TIGROUB/>, T.
PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
SUGAR TRANSPORT 2; 1.
SUGAR TRANSPORT 2; 1.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CAG----CACCCCGACGCCAAGATACCTTGGGCCATCGGCCTAAGCATCGCCTCCACCCTC 1265
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Orobanche ramosa.
Orobanche ramosa.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
Iamiales; Orobanchaceae; Orobancheae;
NCBI_TaxID=46066;
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                         GCCTACGTCGCCTTCTCCATCGGCCTTGGCCCCATCACGTGGGTGTACAGCTCGGAG
                                                                                                       ATCTTCCCGCTCCAGGTGCGCGCGCTGGCTCGCTCGGCGTCGCCCCAACCGCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Delavault P., Simier P., Le Coguic O.;
"Identification of a mannitol transporter, OrMaT1, in Orobanche
                                                                                                                                                                                                                                                                                                     1566 GCCTCGGAATCAGACGAGCCAGCCAAGGAGAAGAAGAAGGTGGAA 1610
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EMBL, AY136668, AANO7021.1; -
SEQUENCE 519 AA, 56257 WW, 97A54DBDDP20047C CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
putative mannitol transporter.
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Matches:
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77.13%
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Best Local Similarity:
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Pred. No.:
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                        CCGAAGAAGAAGGGCAACGTCCGGTTCGCCTTCGCCTGCGCCATCCTCGCCTCCATGACC 188
                                                                       TCCATCCTCCTCGGCTACGATATCGGGGTGATGAGCGGGGCGTCGCTGTACATCAAGAAG 248
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| IleLysSerAsnSerLysLysLeuLeuAlaThrIleAlaValGlyValCysLysThrVal
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(1-513)
JS-10-051-902A-21 (1-2017) x Q9FQX3
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(TrEMBLrel. 21, I
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70.60%
55.32%
38.68%
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01-JUN-2002 (TrEMBLrel
01-JUN-2002 (TrEMBLrel
01-OCT-2003 (TrEMBLrel
Mannitol transporter.
MAT2.
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Best Local Similarity:
                                                                                               GGC 1553
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SEQUENCE 523 A
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1371
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glnGluAlaGlnLeuArgLeuAlaAspIleMetGluAlaAlaGlyLeuProGluAspCys
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                 GCCGTCAACTACGCCATGCTCATGTTCGGCCGCTTCGTGGCCGGCATCGGCGTGGGCTAC
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;

Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;

campanulids; Apiales; Apiaceae; Apioideae; apioid superclade;

Apium clade, Apium.
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                       TTCTACACCTACCTCCCGCAGACCCGCCGCCGGACCCTGGAGGAGATGAGCAAGCTGTTC
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C. STRAIN=cv. Vert d'Elne; TISSUE=Petiole phloem;
A Noiraud N., Pichaud J.-P., Maurousset L., Lemoine R.;
ANDIATA A mannitol transporter from celery.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
C. --SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIM)
C.--SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
R GO; GO: 0005215; P: Transporter activity; IEA.
R GO; GO: 0005215; P: transporter activity; IEA.
R GO; GO: 0005215; P: transporter activity; IEA.
R InterPro; IPR005829; Sub_transporter.
R InterPro; IPR005829; Sub_transporter.
R InterPro; IPR005829; Sugar transporter.
R TIGRAPMS; TIGR0083; Sugar transporter.
R TIGRAPMS; TIGR0083; Sugar transporter.
R PROSITE; PS50860; MES; 1.
R PROSITE; PS50860; MES; 1.
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Transmembrane; Transport.
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| | Search completed: June 3 Job time : 154.5 secs | |
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regectrotroperedgectragececarcacgragergracagerga 1324 COCTCCAGGTGCGCGCTGGCTGCTCGCTCGGCGTCGCCCCACCGCT 1384 SOGICATCICCAIGACCTTCCTGTCGCTGTCCAAGGCCATCACCATCGGCGG 1444 rSerGluValTyrHisThrTrpAlaVal------407

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| Scoring table: IDENTITY NUC Gapop 10.0, | NUC .0 , Gapext 1.0 | |
| Searched: 3470272 s | segs, 21671516995 residues | |
| Total number of hits satis | isfying chosen parameters: | 6940544 |
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| Genembl:* 1. gb ba:* 2. gb ba:* 3. gb lin:* 4. gb con:* 5. gb con:* 6. gb par:* 7. gb ph:* 10. gb ro:* 11. gb ro:* 12. gb ph:* 22. gb ph:* 23. gb ph:* 24. gb ph:* 25. gb ph:* 26. gb par:* 27. gb ph:* 28. gb ph:* 29. gb pr:* 20. gb ph:* 20. gb ph:* 20. gb ph:* 21. gb ph:* 22. gb ph:* 23. gb ph:* 24. gb ph:* 25. gb ph:* 26. gb ph:* 27. gb ph:* 28. gb ph:* 29. gb ph:* 29. gb ph:* 20. gb ph | Embl:* gb ba:* gb ba:* gb_lntg:* gb_ov:* gb_ov:* gb_pv:* gb_pv:* gb_pv:* gb_pv:* gb_vi:* gb_vi:* em_fun:* em_hum:* em_ni:* em_ov:* em_pat:* em_pat:* em_pat:* em_pat:* em_pat:* em_pat:* em_pat:* em_pat:* em_pat:* em_htg_lnv:* | |

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, Y., Naikura, J., Oka, M., Ryu, R., Sugano, S., Sugiama, A., Suzuki, Y. Tsunoda, Y., Ueda, M., Xie, Q., Sydano, S., Yoshimura, A., Matsubara, K. and Murakami, K. Ganome Exploration Research Group in Riken Genome Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Haystsu, M., Hiramoto, K., Inmotani, K., Ishii, Y., Itch, M., Kagawa, I., Kanagawa, S., Katch, H., Kawai, J., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saltoh, H., Sakai, C., Sakazume, N., Sano, H., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Takahashi, F., Takahashi, F., Takahashi, F., Locatloh/Qualifiers
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/db_xref="taxon:39947"
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
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Oryza sativa (japonica cultivar-group) cDNA clone:J033102G08, full
insert sequence.
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Oryza sativa (japonica cultivar-group)
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Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length.cDNA Pool, K. Kishimoto, N. Yazaki, J.
Nagata, T. Kawagashira, N. Doi, K. Kishimoto, N. Yazaki, J.
Ishikawa, M. Yamada, H. Ooka, H. Hotta, I. Kojima, K. Namiki, T. ohnediz. F. Yahagi, W., Suzuki, X., Li, C., Ohtsuki, K., Shishiki, T. and Yamanoto, M.
Fuljumra, T. Ishibiki, J. Kawamata, M. Kobayashi, M. Kodama, T. Kurosaki, T. Kusumegi, T. Lu, M. Masuda, H. Miura, J. Kodama, T. Kurosaki, T. Kusumegi, T. Lu, M. Masuda, H. Miura, J. Kodama, A. Narikawa, R. Niikura, J. Oka, M., Ryu, R., Sugano, S., Sugiyana, A., Suzuki, Y., Tsunoda, Y., Uded, M., Xie, O., Yokomizo, S., Yoshimura, A., Matsubara, K. Mikura, T. Canome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken, Adama, T. Arakawa, T., Hori, F., Hayatsu, N., Hiraoka, T., Hori, F., Ilda, J. Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kangawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kangawa, S., Karoh, H., Kawai, J., Nakamura, M., Nishi, K., Nomina, Y., Kondo, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Osato, N., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Osato, N., Sasaki, D., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Matahashi, F., Yasunishi, A. and Hayashizaki, Y. Towaru, A., Toya, T., Waki, K., Toranon, Ohlalifiers, T., Tomaru, A., Toya, T., Waki, K., Toranon, Ohlalifiers, Y., Towalon, Ohlalifiers, Y., Toya, T., Toya, T., Toya, T., Toya, T., Waki, K., Toya, 
                                                                                                                                                                                 Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
205-6602, Japan (E-mail:sKikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fas.81-29-838-7007
This clone is one of the 26K full-length cDNA clones from japonica
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Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A..
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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(http://www.tigr.org/software/glimmerm/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein databases, nr (ftp://nCBi.nlm.nih.gov/blast/db) and the CDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTS represent the identified CDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified CDNA sequences using BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and 'like protein. A gene without significant homology to any protein but with full-length cDNA or BST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by a single gene prediction program is classified as a probable 'hypothetical' protein according to IRGSP standard. A gene prediction program is also classified as a probable 'hypothetical' protein and is included as a niscellaneous feature of the sequence of COI301 clone (DDBJ: APO04276) at 3 partial sequence of COI301 clone (DDBJ: APO04276) at 3 end. The sequence of COI301 clone (DDBJ: APO04276) at 3 end. The sequence of COI301 clone (DDBJ: APO04276) at 3 end. The sequence was generated by combining Monsanto and RGP-Japan sequencing data. Detailed information of this entry is available at the thin annotation of this entry is the bast of the abstraction of this entry is
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/gene="001301_C12.3"
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/noce="supported by full-length cDNA(s): AK102676"
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/gene="001301_C12.3"
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C20132(E11563), AU163952(E11563), AU097469(S5067),
AU033198(SS067)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="0J1301_C12.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
1. .25270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:39947"
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779. .1103
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                                                                                                                                                                                                                        1510 TGGAGGAGATGAGCAGAGCTGTTCGGCGACACGGCCGCCCCCCGGAATCAGACGAGCAG 1569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1870 GGCTGAGGTTGTGTGTAGCTACTAGAAGTGTCAGTCACGTTGTTGTTAAGAAATGTTT 1929
                                                                                                             Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantaa, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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(bases 1 to 25270)

Sasaki,r. Matsumoto,T. and Yamamoto,K.

Basaki,r. Matsumoto,T. and Yamamoto,K.

Basaki,r. Matsumoto,T. and Yamamoto,K.

Sasaki,r. Matsumoto,T. and Yamamoto,K.

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Tel:81-298-38-7441, Fax:81-298-38-7468)

On Jun 25, 2003 this sequence version replaced gi:21280394.

Genes were predicted from the integrated results of the following:
GENSCAM, (http://CCR-081.mit.edu/GENSCAM.html), FGENESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAGGAGATGAGCAAGCTGTTCGGCGACACGGCCGCCGCCTCGGAATCAGACGAGCCAG
                                                                                                                                                                                                                                                                                                       CCAAGGAGAAGAAGGTGGAAATGGCCGCCACTAACTGATCAAACTAACGGCAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                               1768 CAAAGCTGAGCTCCAGCTCGAGACTTCTTAAAATCATCTTCAAGTACATGGATTTTATTT
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:0J1301_C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.softberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM
(http://rgp.dna.rgfrc.go.jp/RiceHMM/), SplicePredictor
(http://bloinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTGTTAATTAAGCAGTATTGTTGCAGTAATC 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1930 AACTGTTAATTAAGCAGTATTGTTGCAGTAATC 1962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP004185.3 GI:32261236
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LOCUS
DEFINITION
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AUTHORS
TITLE
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REFERENCE
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JOURNAL
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KEYWORDS
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SOURCE

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| codon start=1 | Codon Start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5249 TCCGGTTCGCCTTCGCCTGCGCCATCCTCGCCTCCATGACCTCCATCCTCCTCGGCTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTCGCTGTACATCAAGAAGGACTTCAACATCAGTGACGGGAAGGTGGAGGTTCTCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 CACCGGAGATGGCTTCCGCCGCGCTGCCGGAGGCCGTCGCGCCGAAGAAGAAGAAGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 TCCGGTTCGCCTTCGCCTGCGCCATCCTCGCCTCCATGACCTCCATCCTCCTCGGCTAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3309 GTAACTAATCAAAGCGCATTCACTTCCCGCCCAGCACAGCACGAGCTGCTGCTTCTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5369 AGCATGGGCGCTCATGGCGATGTGCATGTGACCTTGCAGATATCGGGGTGATGAGCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATACTGAACCTCTCGCTCATCGGCTCCTTCGCGGCGGGGGGGACGTCGGACTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GATATCGGGGTGATGAGCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                /gene="0J1301_C12.8"
/note="supported by full-length cDNA(s): AK069022"
complement(19794. .20309)
/gene="0J1301_C12.7"
/note="contains full-length cDNA(s): AK110773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20013. Z048U
/gene="071301_C12.8"
/note="contains EST(8):
D40430(S2406),D15710(C1130A),AU086036(S2406)
contains full-length cDNA(8): AK069022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 2.3e-233;
1; Mismatches 41;
      gene="OJ1301_C12.8"
9581. .21159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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ilarity 93.1%;
Conservative
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                                                                                                                                                                                                                      VLEKTSDTAEEAAERLADIKAAAGIPEELDGDVYTVPKRGSGNEKWKELLISPTPA
KRETLLSGTGIFFÇQASGIDSVVLYSPRVFKSAGITDDKHLLGTTCAVGYTKTLFIL
VATFFLDRVGRRPLLLSSTGMILSLIGGAGGLTVGQHPDAKIPWTGFLSTAY
VAFFSIGGPTTWVSSEIFPLQYRALGCSGAVAARVTSGVISMFELSRAITIG
SFFLYSGIAALAWVFFYTYLPETRGFILEEMSKLFGDTAAASESDEPAKEKKKVEMAA
                                                                                                                          ASLYIKKDFNISDGKVEVLMGILNLYSLIGSFAAGRT6DWIGRRYTIVPAAVIFFAGA
FLMGFAVNYAMLMFGRFVAGIGVGYALMIAPVYTAEVSPASARGFLISPPEVFINFGI
LLGYVSNYAFSRLPLNLGWRIMLGIGAAPSVLLALMVLGMPESPRWLVMKGRLADAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALLMGFSGDYATLMVGRFVAGVGVGYAIMIAPVYTAEISPASSRGFLTSFPEVSINLG
ILLGYVSNYAFARLPLSLGWRVMLGVGAAPSVLLALMVLGMPESPRWLVMKGRLADAK
AVLEKIADTPEBASERLADIKAAAGIPDDLDGDVYTVSKKRGGEEGGVWRELVVSPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMER VLAAVOLHFFQQASGVDSVVLVSPRVFOSAGITGDDOLLGTTCAVGFAKTVFI
LVAAFLLDRAGRRPLLLFSTGGMVFSLVGLATGLTVVGGSPDAQVPSWAVGLCVASIL
AYVAFFSVGLGPMSGVYTSEIFPLRARALGFAVAVACNRVTSGVISMTFLSLSSAITI
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VRLLNPLTRQLTDLPPATTVLDPTSLMISPVHYLLHVLTVHGAGLADGSATVVVYFEN
ARKLAAAKFGDERWTVVEPDASFASVSSFAGRFYCATRHAIRPVIVEVRTTDHRLPPQ
                                                                                                  translation="MASAALPEAVAPKKKGNVRFAFACAILASMTSILLGYDIGVMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tzānslation="MPESTKLTAMAVDPKKKNASYAFTCAILASMASIILGYDIGYMS
GASLYIKKDLKITDVQVEILMGILNIYSLVGSFAAGRTADWIGRRFTVVPAAAFFPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MAKRARTLTGDHLRSSSSNQAPSWGAKRARSGSALRDRSLPDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="probably inactive due to including stop codon(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpc_type_terminal repeat"

complement(19137. .20909)
/gene="0.013.01_c12.7"

complement(19137. .20909)
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19581. .21159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11758. .12731

| John (11758. .12731)

| John (11758. .1894,11990. .12071,12243. .>12731)

| John (11758. .11894,11990. .12071,12243. .>12731)

| John (11758. .11894,11990. .12071,12243. .12731)

| John (11758. .11894,11990. .12071,12243. .12731)

| John (11758. .11894,11990. .12071,12243. .12731)
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complement(join(<7647. .9067,9210. .>9324))
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   sorbitol transporter'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(12995. 17622,18451. 19187)

Gene= 00/1301_C12.6"

12995. 13731_C12.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="5' Terminal repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                        complement (7647.
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| 1168 TCTCCCTCATCGGCCTCGGCCGGGCTCACCGTCGCCAGCACCCCGACGCCAGA 1335 1276 TCTCCCTCATCGGCCTCGGCCGGCCTCGCTCGGCCAGCACCCCGACGCCAGA 1335 1276 TCTCCCTCATCGGCCTCGGCCTCGCTCGGCCTCGCCTACGTCGCCCAGCCCCAGA 1335 1281 | RESULT 6 BT009264 BT009264 CCCUS DEFINITION Triticum aestivum clone wlk8.pk0001.all:fis, full insert mRNA ACCESSION Triticum aestivum clone wlk8.pk0001.all:fis, full insert mRNA ACCESSION BT009264 BT1CDNA FLI CDNA FREFERENCE I (bases 1 to 2109) AUTHORS TINGEY, S. V. Molters, P. Powell, W., Dolan, M., Miao, GH., Caraber, N.R., Hanafey, M.K. and Hainey, C.F. TITLE Direct Submission JOURNAL COMpany, I Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, COMpany, I Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, COMPAND COMPAND FEATURES FEATURES FOOTE TRITICUM FOOTE | Query Match 55.5%; Score 1120.2; DB 8; Length 2109; Best Local Similarity 80.1%; Pred. No. 4.3e-143; Matches 1359; Conservative 1; Mismatches 319; Indels 18; Gaps 3; |
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| B CACCGGAGATGGCTTCCGCCGCGCCGCGCCGCGCCGAAGAAGAAGAACGAAC | 10.06 TCGGCACGCGCGCGGGGGGCGCGCGAGGGCCCCGCGGACGCCAAGGGGGG | 1108 TCTTCATCGACGCGTCGGCGGCGCCGCTGTTGCTGGGCAGCACGGGCGGG |

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| | RESULT 7 LOCUS LOCUS DEFINITION Sequence 25 from patent US 6383776. ACCESSION AR208577 VERSION AR208577 GI:21509767 VERSION AR208577.1 GI:21509767 LOCALDAN AR2085 LOCALDAN AR208577.1 GI:21509767 AUTHORS LOCALDAN AR208577.1 GI:21509767 LOCALDAN AR208577.1 GI:21509767 AUTHORS LOCALDAN AR208577.1 GI:21509767 LOCALDAN AR208577.1 GI:21509767 AUTHORS LOCALDAN ARXIVENES LOCALDAN A | Query Match 54.3%; Score 1094.6; DB 6; Length 2089; Best Local Similarity 79.1%; Pred. No. 1.3e-139; Indels 18; Gaps 3; Matches 1343; Conservative 1; Mismatches 335; Indels 18; Gaps 3; Qy 84 GGACGACGACGACGACGCCGCACGCACGCCGACGCCGAAGAA |
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| 84 GCACCACCGGAGATGGCTTCCGCCGCGAGCCGTCGCCCGAAGAAGAAGGCC | | AAACATTCTTGGGCACCACTTGGCGGTGCACCACAGAGGGTTTTCATCTTGTTG 110 |

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| 1205 GAGAAGATCACCTGGGCCATCGTGCATCTTCTGCATCATGGCCTACGTGGCCTTCTCCTGCATCATGGCCCTACGTGGCCTTCGGGGGTGCTCCGGAGATCTTCCCGCTCCATCACCTGGGGTGTACAGCTCGGAGATCTTCCCGCTCCAGTGCACCTCAGTGGGCTTACAGTTCAGCTCGGAGATCTTCCCGCTCAGTGCACCTCAGTGGGCTTACAGTTCAGCTCGGAGATCTTCCCGCTGCACCTGCAGTGCACCTGCAGCTGCACCTGCAGCTGCACCTGCAGCTGCACCTGCAGCTGCACCTGCAGCGGTGACCTCTCTCT | Qy 1461 TCCGGCATCGCCTGGCTGGTTCTTCTACCTCCCGGAGACCCGCGGC 1520 Db 1445 GCCGCATCGCTCATTCGCATGGTTCTTCTTCGCCTACCTGCGGGGAGACCGGGGG 1504 Qy 1521 CGGACGCTGGAGGAGATGAGCAGGTGTTCGGCGACACGGCCGCCGCCGCCGCGGCGCGCGC | Db 1565 GCGGAAGCCGACGACGCGGGAAAGGCGCGAAATGGCCGCCACCACCACCACCACCACCACCACCACCACCACC | 1746 GGAGGGCGGC 1762 1745 GGAGGGCGGC 1761 1745 GGAGGGCGACGCAAGC 1761 | | KEYWORDS FILCONA, oligo capping. SOURCE Oryza sativa (japonica cultivar-group) ORGANISM Oryza sativa (japonica cultivar-group) Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermarophyta, Aggnollophyta, Liliopsida, Poales, Poaceae; | Ehrhartoideae; Oryzeae; Oryza. REFERENCE 1 AUTHORS The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, | <pre>Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishwaya, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohndaikwa, M., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fulimuxa, T., Suzuki, Y., Tsunoda, Y.,</pre> | <pre>Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sudiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Marsubara,R., RIKEN:, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,</pre> | Hara, A., Hashldume, W., Hayatsu, M., Imotanı, K., Ishli, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Salto, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y. | Æ |
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uku. intp://comadu.ana.airrc.go.jp/cuw/
NTAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Rawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Nagata,T., Rawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
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Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
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Kis,Q., Yokomizo,S., Yoshimura,A., Narkanea,R., and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Alzawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hiracka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Kondo,H., Kawai,J.,
Kishikawa-Hirozane,T., Matayama,T., Myazaki,A., Murata,M.,
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Yasunishi,A., and Hayashizaki,Y.
                                                                                                 CE Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hayatsu, N., Hamamta, K., Hayashida, K., Ishibiki, J., Ishida, Y., Ishikawa, M., Icoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kodama, T., Kojima, K., Kojima, Y., Misumaci, J., Miyazahi, M., Kodama, T., Kushimoto, N., Miwazahi, M., Masuda, H., Matsubara, K., Matsubara, K., Murakami, K., Murakami, K., Matsupama, T., Mikura, J., Miyazaki, A., Miyazaki, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Noka, M., Otano, Y., Ryu, R., Saitoh, H., Satoh, K., Sakai, C., Sakai, K., Satoh, M., Sano, H., Sasaki, D., Satoh, K., Sakai, C., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugamo, S., Sugiyama, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugami, M., Yamada, H., Yamamoto, M., Yasunishi, A., Waki, X., Xie, Q., Yahagi, W., Yamamada, H., Yamamoto, M., Yasunishi, A., Waki, X., Xie, Q., Yahagi, W., Yamamada, H., Yamamoto, M., Yasunishi, A., Waki, Y., Yan, Japanishi, A., Hoses, I., Inakas, I., Tomaru, A., Toya, T., Tamaka, T., Tomaru, A., Toya, T., Yamamoto, M., Yasunishi, A., Waki, Y., Yan, J., Johase, I., Tohasa, I., Yamamoto, M., Yasunishi, A., Waki, Y., Yan, J., Japan, J., Japan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-72M-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fas:81-29-838-7007, This clone is one of the 32K full-length cDNA clones from japonica

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    /organism="Oryza sativa (japonica cultivar-group)"

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Kikuchi, S.
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AUTHORS
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| Db 1375 CCTGTCCCTCTCCAAGGCCATCACCATCGGCGGCAGCTTCTTCCTCTACTCCGGCATCGC 1434 | OY 1472 CGCGCTCGCCTGGGTGTTCTTCTACACCTACCTCCCGGAGACCCGGGCGGG | | OY 1586 AGCCAAGAAGAAGAAGAAGAAATGGCGCACTAACT 1626 | RESULT 10 | Z | ACCESSION BT009301.1 GI:32128852 VERSION BT009301.1 GI:32128852 KEYWORDS FLI CDNA. SOURCE Trificum aestivum (bread wheat) | OKGANISM ILLLLund asslivationiae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum. | Tingey.S.V., Wolters,P., Powell,W., Dolan,M., Miac,GH., Tingey.S.V., Wolters,P.X. and Hainey,C.F. Caraher,N.X., Hanafey,M.X. and Hainey,C.F. Direct Submission | JOURNAL Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA Location/Qualifiers | source 1.1872 /organism="Triticum aestivum" /mol type="mRNA" /db_xref="taxon:4565" | /Clone="wimi.pk0012.fl: ORIGIN | Query Match Best Local Similarity 77.7%; Pred, No. 4.2e-125; Matches 1192; Conservative 1; Mismatches 341; Indels 0; Gaps 0; | QY 99 GCTTCCGCCGCGCTGCCGGAGCCGTCGCGCGAAGAAGAAGGGCAACGTCCGGTTCGCC 158 | 159 | 219 ATGAGGGGGGTGCTGTACATCAAGAAGGACTTCAACATCAGTGACGGGAAGGTGGAG | m m | Db 308 ATCATGATGGGCATCCTGAGGGGTGTACGGGGTCCTTCGGGGGGGG | 368 TCGACTGGGTCGGCGGCGCGCGTCGTCTTCGCGGCCGCCATCTTCACCACCGGC 42 | Qy 399 GSGTICCTCAIGGGGTICGCGTCAACTACGCCAIGCTGTICGCCGCTTCGTGGCC 458 | ON 459 GGCATCGGCGTACGCGCTCATGATCGCGCCGGTGTACACCGCCGAGGTGTCGCCG 518 |

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Direct Summission

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Submitted (120.5EP-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2 Tsukubai, Ibazaki 305-8602, Jupan

(B-mail:teasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Jun 25, 2003 this sequence version replaced gi:21280394.

Genes were predicted from the integrated results of the following: (http://www.softbery.com/), GeneMark.htmm

(http://www.softbery.com/), GeneMark.htmm

(http://www.igir.org/cdb/glimmerm/glmr_form.html), RiceHWM

(http://www.tigr.org/cdb/glimmerm/glmr_form.html), RiceHWM

(http://www.tigr.org/cdb/glimmerm/glmr_form.html), RiceHWM

(http://www.tigr.org/stckware/glimmerm/lb SplicePredictor

(http://www.tigr.org/stckware/glimmerm/lb SplicePredicted

(http://www.tigr.org/stckware/glimmerm/lb SplicePredicted

(http://www.tigr.org/stckware/glimmerm/lb SplicePredicted

(http://www.tigr.org/stckware/glimmerm/lb SplicePredicted

(http://www.tigr.org/stckware/glimmerm/lb SplicePredicted

A gene with the corresponding DDBJ accession no.

A gene with identity or significant homology to any protein but with full-length copy to any protein but with full-length copy to any protein but with full-length copy or solesified as a probable 'hypothetic
                                                                                                                                                                                                                            ARUU4185
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7,
BAC clone:0J1301_C12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This is a partial sequence of 001301 C12 clone. This sequence of 001301 C12 clone. This sequence AP004276)at 5' end and an overlap with 001127 E01(DDBJ: AP003747) at 3' end. The sequence was generated by combining Monsanto and RGP-Japan sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Dukaryota, Viridiplantea; Streptophyta, Embryophyta, Tracheophyta;
Spernatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki,T., Matsumoto,T. and Yamamoto,K.

oloyza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC clone:OJ1301 cl2.

Published Only in Database (2001)

2 (bases 1 to 25270)

Saski,T., Matsumoto,T. and Yamamoto,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://rgp.dna.affrc.go.jp/GenomeSeg.html
Location/Qualifiers
    1599 AAGAAGGTGGAAATGGCCGCCACTAACTGATCAA 1632
                                                                         1628 AAGGCGAAAGTAGGGGAGATGAACTAGTGAGCTA 1661
                                                                                                                                                                                                                                                                                                                                                                                   AP004185
AP004185.3 GI:32261236
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AP004185/c
                                                                                                                                                                                                                                                                                                      DEFINITION
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FLMGFAVNYAMLMFGRFVAGIGVGYALMAPVYPTAVSPASARGFLTSFPEVFINFGI
LLGYVSNYARSRLENLGRRIMLGGTGAAPSVLLALMVLGMPESPRWIVMKGRLADAKV
VLEKTSDTAREBAABRLADIKAAAGIPEELDGDVVTVPKRGSGNEKRVWKELILSPTPA
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AVLEKIADTPEBEASERLADIKAAAGIPDDLJGGDVVTVSKKRGGEBGGVWRELVVSPTP
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AYVAFFSVGLGPMSGVYTSEIFPLRARALGFAVAVACNRVTSGVISMTFLSLSSAITI
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VATFFLDRVGRRPLLLSSTGGMILSLIGLGAGLTVVGQHPDAKIPWAIGLSIASTLAY
VAFFSIGLGPITWVYSSEIFPLQVRALGCSLGVAANRVTSGVISMTFLSLSKAITIGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this category is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C20132 (E11563), AU163952 (E11563), AU097469 (S5067),
AU033198 (S5067)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contains full-length cDNA(s): AK059423, AK102676"
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join(<779. 940,1011. .>1103)
gene="0J1301_C12.1"
note="start and end point are not identified"
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gene="OJ1301_C12.1"
note="predicted by GENSCAN etc."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted by GENSCAN
                                                                                                           clone="0J1301_C12"
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REDWSSIGNGPAWISERVLAGDDVADVADVEBERGHRVGPTABGLLJLLLDEATFA
VRILNPLTRQLTDLPPATTVLDPTSLMISPVHYLLHVLTVHGAGLADGSATVVVYFEN
ARKLAARKGODERWHVVEPDASFASVSSFAGRFYCATRHAIRPVIVERTTDHRLPPQ
LVVVAKLAGVPSFPRNC"

10011(1295): 11762,18451. 19187)

/genne="Oli301">12.6"
12395: 13731

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QppsapprQptlppGvspltarassrapcrpppppavpatccllprlpppasCyHlrr
CELRRSETCLAMTSASSASRRTAPRVPPPESPAPDPATGRPDQPPRGPNPPFAWPDS
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complement(19794. 20309)
/gene="0J1301_C12."
/note="contains full-length cDNA(s): AK110773"
                                                                                                                                       11758. .12731

Join (-11758. .11894,11990. .12071,12243. .>12731)

Join (-11758. .11894,11990. .12071,12243. .>12731)

Join (-11758. .11894,11990. .12071,12243. .12731)

Join (11758. .11894,11990. .12071,12243. .12731)

Join (-11758. .11894,11990. .12071,12243. .12731)

Join (-11758. .11894,11990. .12071,12243. .12731)
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/note="contains ESTY(6):
040430(52406),D15710(C1130A),AU086036(S2406)
contains full-length cDNA(s): AK069022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 985.8; DB 8; Length
Pred. No. 7.7e-125;
1; Mismatches 248; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pseudogene, Fourf gag/pol protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="hypothetical protein"
protein_id="BAC83312.1"
db_xref="G1:34393632"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18451. .19187
/gene="0J1301_C12.6"
/noce="3 Terminal repeat"
/rpt_type=terminal
complement(19137. .20909)
/gene="0J1301_C12.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="5' Terminal repeat"
/rpt type=terminal
1387. 17652
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product="unknown_protein"
protein_id="BAC83313.1"
/db_xref="G1:34393633"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (19137, .20909)
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/gene="GJ1301_C12.8"
19581. .21159
/gene="GJ1301_C12.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="OJ1301_C12.6"
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| OY 1404 ATGACCTTCCTGTCGCTGTCCAAGGCCATCACCATCGGGGGCAGCTTCTTCCTCTACTCC 1463 Db 7868 ATGACCTTCCTGTCGCTCTCCCAGGGCCATCACCATCGGGGGCAGCTTCTTCTCTCTACTCC 1463 OY 1464 GGCATCGCTGGCTCTTCTTCTTCTACCTCCCCGGGAACCCGCGGGCGG | | |

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clone="P0458E05"
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/note="5' LTR"
25856. .30421
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Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Submission

Auricled (19-NOV-2001) Takuji Sasaki, National Institute of Submission

Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Teukuba, 1Daraki; 305-8602, Japan

(5-mai): Isasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7468)

On Jul 17, 2002 this sequence version replaced gi:19773518.

Genes were predicted from the integrated results of the following:

Genes were predicted from the integrated results of the following:

Genes were predicted from the integrated results of the following:

Genes were predicted from the integrated results of the following:

Genes were predicted from the integrated results of the following:

Genes were predicted from the integrated results of the following:

GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor

(October 1998 version). The genomic sequence was searched against

NOBI NonRedundant Protein database, uith BLASTP2.0. ESTS represent

KGP, Protein homologies of the coding regions were searched against

NOBI NonRedundant Protein database with BLASTP2.0. ESTS represent

the identified CDNA sequences using BLASTN 2.0 with the

corresponding DDBJ accession no. and RGP clone in.

A gene with identity or significant homology to any protein name to indicate the homology to any protein name to indicate the homology to any protein name to indicate the homology to any protein but with a gene prediction program

is classified based on the protein and verlap with Polsasified as an 'unknown' protein. A gene predicted with a gene prediction of partial sequence) is classified as an 'unknown' protein of Polsasified as an overlap with Polsasified as any ender and any everlap with Polsasified as any ender and any everlap and assembly quality

The criminal of the sequence of Polsasified as any ender any e
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Katayose,Y., Wu,J., Niimura,Y., Cheng,Z., Nagamura,Y.,
Antonio,B.A., Kanamori,H., Hosokawa,S., Masukawa,M., Arikawa,K.,
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Yano,M., Jiang,J., and Gojobori,T., Ito,H., Hahn,J.H., Kim,H.I., Eun,M.Y.,
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
                                                                                                        PLN 27-NOV-2003
                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                          APU04365 193577 bp DNA linear PLN 27-NOV-200
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome l,
PAC clone:P0458E05.
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// Organism="Cryza sativa (japonica cultivar-group)"
// Mol. type="genomic DNA"
// Cultivar="Nipponbare"
// Cultivar="Nipponbare"
// Chromosome="1"
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KEYWORDS
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/ COGGOT = SEATCH
/ COGGOT = SEATCH
/ COGGOT = SEATCH
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TGGAHPSSPSSRRSRRPRRRRRRRRRRRRRRRRRRRRRRRRDPPPRAIKIELAPSSSLSSVADDLRP
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BAEPMIQEMDELGLGESIIDEEYLACLGNLPHGPPRPDTKTKLQGGQLHDLYIRHTVY
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DGQTERVNQILEDMLRACALDFBGTWDRCLPYAEFSYNNSYQASIQMSPNEAMFGRKC
RTPLCWNEVGEALVFGPDILKSAEEQVKLIRERLKTAQNRQKNYADNRRRDLEFEKGD
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QLKKCLRVPEEQVPLGNIELEKNLTYKERPIKVLEEVERQTRRKTIKFYKVQMSNHSE
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Join(1748. .1991,2570. .2750,2997. .3243,5685. .5813,
5922. .6140,6199. .6213)
Gene="P0458E05.1"
                                                                                                        join(1748. .1991,2570. .2750,2997. .3243,5685. .5813,
5922. .6140,6199. .6213)
/gene="P0458E05.1"
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product="putative polyprotein"
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17098. .20885
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12336. .17054
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25856. .30421
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/brotein_id="BAC05605.1"
/db_xreff="G1:21902057"
/translation="MDAAGTTKISDFGLAKLLQPDQTRTFTSVRGTRGYLASEWYRGA
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/gene="P0458E05.6"
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pseudogene, putative retroelement pol polyprotein"
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60240. .60320)
/gene="P0458E05.6"
/codon_start=1
/product="putative chromosome condensation factor"
/protein id="BAC05606.1"
/db_xref="G1:21902058"
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/gene="pod5805.4"
/gene="pod5805.4"
/gene="pod58505.4"
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Pred. No. 1.9e-114;
1; Mismatches 269;
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/gene="P0458E05.5"
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/note="problem:
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/note="3' LTR'
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| 14 | | ETCTICTICTICACCIACCICCGGAGACICGIGGACGCACGCICGAGCAGATG 149866 | ORIGIN | z |
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| Qy 1539 Db 149865 | 1539 AGCAAG | AGCAAGCTGTTCGGCGAAACGGCCGCCGCCTCGGAATCAGACGAGCCAGCC | Query Best I Matche | Query Matc Best Local Matches 9 |
| RESULT 14 | | | δ | 20 |
| AC116426/c LOCUS | AC116426 | 155037 bp | qC | 8901 |
| DEFINITION | Genomic OSJNBb00 | quence P18, fr | ò | 26 |
| ACCESSION VERSION | AC116426 AC116426.1 | .1 GI:19774446 | qq | 8895 |
| SOURCE | Oryza sativa | iva (japonica cultivar-group) | ò | 32 |
| CRGANISM | Oryza sativa Eukaryota; Vi | iva (japonica cultivar-group) in Viridiplantae, Streptophyta; Enbryophyta; Tracheophyta; | qq | 8889 |
| acka aaaa a | Spermarc Ehrhartc | Spermatophyta; Magnollophyta; Lillopsida; Foales; Foaceae; Ebrhartolodeae; Oryzeae; Oryza. 1 /knoon 1 to 155001 | ò | 38 |
| AUTHORS | McCombie | W.R., Spiegel,L., de la Bastide,M., Preston,R., Kuit,K., | qq | 8883 |
| | Baker, J. | reifaic,n., Nascimenc,b., zucavein,i., bailja,v., beil,m., basker,d., Santos,b., Miller,B., Katenberger,F., Muller,S., bilar, b., bilar,B., bilar, | δ | 44 |
| (((| Dedhia, h | rang, c., Dire, s., O Shaughinessy, ra. ranker, b. and | DP | 8877 |
| STILL | Genomic OSJNBb00 | Genomic sequence for Oryza sativa, Nippondare strain, clone SOSNBBOOSSPIB, from chromosome 3, complete sequence | ò | 50 |
| REFERENCE | Unpublished 2 (bases 1 | ned = 1 to 155037) | qq | 8871 |
| AUTHORS | McCombie Direct S | | ò | 56 |
| COURNAL | Spring F | Submitted (28-MAK-2002) Lita Annenberg Hazen Genome Center, Cold Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor, | Д | 8865 |
| COMMENT | This sec | once was finished as follows unless otherwise noted: all | ò | 62 |
| | chemistr | were either double stranged or sequenced with an allegate or covered by high quality data (i.e., phred quality >= | q | 8859 |
| | as compr | 30); an arcempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least | δλ | 68 |
| | assembly | And succione of more than one Mis succione; and the | qq | 8853 |
| | (AC11568 | Nubboudskil overlaps inished clone Osunbauusiui.)) from base 1 to base 94350. The overlap is from base | ò | 74 |
| FEATURES | 86812 50 | <pre>86412 to Dase 181163 on USONBaUUYLUIL. Location/Qualifiers 1 155.07</pre> | QQ | 8847 |
| SORIOR | | /organism="Oryza sativa (japonica cultivar-group)" | ò | 80 |
| | | /mol_cype="genomic DNA" /cultivar="Nipponbare" /dh vref="havon:1904" | Ob | 8841 |
| | | / Chronosome = 13: | λō | 85 |
| | 4 | /clone="UsuMbD0Uskri8" /clone lib="EcoRi" // clone lib="EcoRi" | QQ | 8835 |
| ار | reacute | /note="We believe the assembly to be correct. The | ΟŸ | 91 |
| | | sequence is covered by a FCR product which was amprimed with a high fidelity polymerase. There is additional consequent by a single subclone with mality helps physelegin " | d d | 8829 |
| misc_f | feature | 16.142. 16.24 4 1 16.24 4 1 16.24 1 | λ̈́O | 97 |
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| , t | 4 5 5 7 7 | | ò | 103 |
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| | | Sequence is a mononucleoride (c) repeat in which the exact number of Cs is unknown. One subclone in the region spans into unions accommance or both either." | ò | 109 |
| misc_f | misc_feature | 1100 unique sequence on both states. 136662, 137340 " " h) the amount); to be correct the | qq | 8811 |

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Sequence is a mononucleotide (C) repeat with a single unique base (A) followed by another monoucleotide (C) repeat. A single subclone spans the region into unique sequence on both sides."
JSZ459. JSZ479
JOSZ459. JSZ479
JNOTE-WW believe the assembly to be correct. The sequence is a monoucleotide (C) repeat flanking a single unique base (A) which is followed by an additional monouncleotide (C) repeat. A single subclone spans through to unique sequence on both sides."
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                                                                                                                                                                                                                                                                                sequence is a dinuclectide (TÅ) repeat followed by a dinuclectide (CÅ) repeat. Three subclones span into unique sequence on both sides." 132738. ... 132738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Gaps
                                   /note="We believe the assembly to be correct. The sequence is a dinucleotide (TA) repeat followed by a dinucleotide (CA) repeat. Four subclones span into 53504. 53580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 759.4; DB 8; Length 181163;
Pred. No. 4.8e-94;
1; Mismatches 357; Indels 9;
                                                                                                                                                                                                                                        /note="We believe the assembly to be correct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGTGCGCGCGCTGGGTGCTCGCTCGGCGTCGCCGCCAACCGCGTCACCAGCGGCGGCGTC 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCTCCATGACCTTCCTGTCGCTGTCCAAGGCCATCACCATCGGCGGCAGCTTCTTCCTC 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACTICOGGCATCGCCGCGCCTGGCTGTTCTTCTACACCTACCTCCGGAGACCCGC 1517
GGGATAATCCTCTCCCTCATCGGCCTCGGCGCCGGGCTCACCGTCGTCGGCCAGCACCCC 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryzae;
I (bases 1 to 181163)
McCombie,W.R., de la Bastide,M., Spiegel,L., Preston,R.,
Berraro,K., Kult,K., Nascinento,L., Zutaven,T., Balija,V.,
Bell,M., Baker,J., Santos,L., Miller,B., Katzenberger,F.,
Muller,S., King,L., Yang,C., Dike,S., O'Shaughnessy,A., Palmer,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NY 11724, USA

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (22-MAR-2002) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
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                                                                                                                                                                  GACGCCAAGATACCTTGGGCCATCGGCCTAAGCATCGCCTCCACCCTCGCCTACGTCGCC
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87693 GGCAGGAGCCTGGAGGACACCGTCAAACTCTTCGGCGGC 87655
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/clone_lib="HindIII"
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AC115687.1 GI:19683096
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- 2004 Compugen Ltd.
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ALIGNMENTS

ACA32312 ACA38748 AAI99683_37 AAF55869

ADC07783 AAZ32199

ADA48271

1752 1572 1577 1577

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The present invention relates to the isolation of plant polynucleotide sequences encoding an Arabidopsis thaliana-like sugar transport protein. The polynucleotide or beta wilgaris-like sugar transport protein. The polynucleotide sequences are useful for altering the level of sugar transport proteins in plants, i.e. for control of carbohydrate transport and distribution in
                                                                                                             Beta vulgaris-like sugar transport protein; carbohydrate transport; filling; annual field crop; plant; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding plant sugar-transport proteins, useful fo
preparing transgenic plants with altered carbohydrate distribution.
                                                                                                                                                                                                                             Beta vulgaris-like sugar transport
                                                                                    Rice contig encoding Beta vulgaris-like sugar transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                 SV;
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                                                                                                                                                                                Location/Qualifiers
96. 1628
7*tag= a
/product= "Rice Beta
protein"
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ABK51972 standard; cDNA; 2017 BP.
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                                                       (first entry)
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P-PSDB; AAU97211.
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Arabidops Nucleotid Nucleotid Nucleotid Corn cDNA

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ABL41879 ADA49209

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426 397.4 387.6 343.6 325.4 325.3

Nucleotid Nucleotid

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                                                                                                                                                                                       Beta vulgaris-like sugar transport protein; corn; rice; wheat; plant sugar transport protein; carbohydrate transport; soybean; carbohydrate distribution; plant; gene; ss.
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     Query Match 100.0%; Score 2016.6; Best Local Similarity 100.0%; Fred. No. 0; Matches 2017; Conservative 0; Mismatches
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                                                                                    ABX93208 standard; cDNA; 2017
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HITZ W D.
KINNEY A J.
TINGEY S V.
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14-APR-1999;
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The present invention relates to the isolation of plant polynucleotide sequences encoding an Arabidopsis thalians—like sugar transport protein or Beta vulgaris-like sugar transport protein. The polynucleotide sequences are useful for altering the level of sugar transport proteins in plants, i.e. for control of carbohydrate transport and distribution in plants, i.e. for control of carbohydrate transport and distribution in plant cells, e.g. during grain filling of annual field crops (e.g. corn, rice, soybeans, and wheat), and, for studying carbohydrate flows and sugar transport. The polynucleotide sequences can also be used to isolate obsessort sequences and genes that encode homologues of the new proteins. The protein
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                            sugar transport
                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding plant sugar-transport proteins, useful fo
preparing transgenic plants with altered carbohydrate distribution.
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                                                            codon
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                         /product= "Wheat Beta vulgaris-like
protein"
/note= "This sequence lacks a start
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Pred. No. 1.9e-177;
1; Mismatches 335;
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Pred. No. 1.9e-177;
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The present invention relates to the isolation of Arabidopsis thalianalike or Beta vulgaris-like sugar transport proteins, and the polynucleotide sequences encoding them. The plant sugar transport proteins of the invention have been isolated from corn, rice, soybean, and wheat. The polypeptides of the invention may be used for altering the level of expression of a sugar transport protein in a host cell, by transforming a host cell with a chimeric construct encoding all, or a portion of the sugar transport protein, in sense or antisense orientation. Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants. ABX93206-ABX92311 represent cDNA sequences encoding Beta vulgaris-like sugar transport proteins
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Beta vulgaris-like sugar transport protein; corn; rice; wheat; plant sugar transport protein; carbohydrate transport; soybean; carbohydrate distribution; plant; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of plant polynuclectide sequences encoding an Arabidopsis thaliana-like sugar transport protein or Beta vulgaris-like sugar transport protein. The polynuclectide sequences are useful for altering the level of sugar transport proteins in plants, i.e. for control of carbohydrate transport and distribution plant cells, e.g. during grain filling of annual field crops (e.g. corn, rice, soybeans, and wheat), and, for studying carbohydrate flows and sugar transport. The polynuclectide sequences can also be used to isolate cDNA sequences and genes that encode homologues of the new proteins. The present sequence encodes a wheat Beta vulgaris-like sugar transport
              ---GACACGCCCCCCCCCCGCAATCAGACGAGCC 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding plant sugar-transport proteins, useful fo
preparing transgenic plants with altered carbohydrate distribution.
                                                                                                                                                                                                                                                                                                    transport
                                                                                                                                                                                Wheat cDNA clone wlm1.pk0012.hl encoding sugar transport protein
                                                                                                                                                                                                                plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 981.6; DB 6; Length 1872;
Pred. No. 3.4e-158;
1; Mismatches 345; Indels 0;
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                                                                                                                                                                                                                                                                                                   Beta vulgaris-like sugar
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                                                            CGCAGCCAAGGAGAAGGTGGTGGAACTGCCTAGCAGCAAGT
                                        AGCCAAGGAGAAGAAGGTGGAAAATGGCCGCCACTAACT
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Best Local Similarity 77.4%;
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P-PSDB; AAU97214.
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proteins of the invention have been isolated from corn, rice, soybean, and wheat. The polypeptides of the invention may be used for altering level of expression of a sugar transport protein in about cell, by transforming a host cell with a chimetic construct encoding all, or a portion of the sugar transport protein, in sense or antisense orientation. Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants. ABX93206-ABX93211 represent cDNA sequences encoding Beta vulgaris-like sugar
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                                                                                                                                                                                     Score 981.6; DB 7;
Pred. No. 3.4e-158;
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(HITZ/) HITZ W D.
(KINN/) KINNEY A J.
(TING/) TINGEY S V.
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P-PSDB; ABU08339.
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The present invention relates to the isolation of plant polynucleotide sequences encoding an Arabidopsis thaliana-like sugar transport protein or Beta vulgaris-like sugar transport protein. The polynucleotide sequences are useful for altering the level of sugar transport proteins in plants, i.e. for control of carbohydrate transport and distribution in plant cells, e.g. during grain filling of annual field crops (e.g. corn, rice, soybeans, and wheat), and, for studying carbohydrate flows and sugar transport. The polynucleotide sequences can also be used to isolate present sequences that encode homologues of the new proteins. The present sequence contig assembled from various soybean cDNA clones encodes a Beta vulgaris-like sugar transport protein
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                                                                                                                                                                                   New nucleic acid encoding plant sugar-transport proteins, useful for preparing transgenic plants with altered carbohydrate distribution.
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ate transport; grain filling; annual field
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The present invention relates to the isolation of Arabidopsis thalianalike or Beta vulgaris-like sugar transport proteins, and the polynucleotide sequences encoding them. The plant sugar transport proteins of the invention have been isolated from corn, rice, soybean, and wheat. The polypeptides of the invention may be used for altering the transforming a host cell with a chimeric construct encoding all, or a portion of the sugar transport protein, in sense or antisense orientation. Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants. ARX93206-ABX93211 represent CDNA sequences encoding Beta vulgaris-like sugar
                                                                                                                                                                                                                                                                                                                                           transport proteins and nucleic acid encoding the producing transgenic plants having altered levels of
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Pred. No. 6.7e-89;
2; Mismatches 510; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1853 BP; 457 A; 434 C; 448 G; 513 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                               Tingey SV;
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 34-35; 56pp; English.
                                                                                                                                                                                                                                                               Kinney AJ,
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                                                                                               17-JAN-2002; 2002US-00051902.
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Best Local Similarity 63.6%;
Matches 909; Conservative
                                                                                                                                                                                                                                                                                                                                                 Novel plant sugar transport
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P-PSDB; ABU08337.
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KINNEY A J
TINGEY S V
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14-APR-1999;
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The present sequence encodes a polypeptide which is a transporter of a linear polyol. DNA encoding linear polyols is used to produce a selection system for transformed cells, based on the use of polyols as the only carbon source. It is also used to produce transgenic plants with increased resistance to pathogens and salt stress. The use of a linear polyol for selection eliminates the need for toxic selection reagents souch as antibiotics. Also, the linear polyol is not essential for the plant, once selection has been made. The linear polyol has a main chain of 5-8, preferably 6, carbon atoms and is selected from sorbitol, dulcitol, galactitol, (myo-)inositol, ribitol, or xylitol 211 257 317 331 377 391 437 451 497 New polyol transporter protein from plants, for selecting transformed cells and for imparting pathogen and salt-stress resistance to plants. 318 aaradgagrirchagredgaarerraaacareracheerecherredgererredgagered GIICGCCIICGCCCAICCICGCCICCAIGCCICCAICCICCICCICGGCIACGAIAI erinectrinactricica acridectricia reservate e introcura de la compania del compania del compania de la compania del compania del compania de la compania del compania d CGGGGTGATGAGCGGGGCGTCGCTGTACATCAAGAAGGACTTCAACATCAGTGACGGGAA regacitaticacidecaaraarciacercaaagaagacigecacarragigacacaca GGTGGAGGTTCTCATGGGCATACTGAACCTCTACTCGCTCATCGGCTCCTTCGCGGCGGG rdaactrocaaridgardgacdacdracaccardgrarragcragcaarcrorr CGCGGGGGGGGTTCCTCATGGGGTTCGCCGTCAACTACGCCATGCTCATGTTCGGCCGCTT cerrececeaciacircarecerrirececacaaciaecarirereareciarecerrir CGTGGCCGGCCATCGGCGTGCGCTACGCGCTCATGATCGCGCCGGTGTACACCGCGAGGT reraacaddaaraddrerredrirardcacrrardarcecaccrerracacrecadaddr Gaps polyol transporter; carbon source; plant; stress; sorbitol; dulcitol; galactitol; Э, DB 6; Length 2056; Sequence 2056 BP; 570 A; 374 C; 444 G; 667 T; 0 U; 1 Other; Indels Nucleotide sequence of a linear polyol transporter. 23.7%; Score 477.2; DB 6; 59.2%; Pred. No. 3.5e-72; iive 1; Mismatches 569; Disclosure; Page 41-42; 66pp; French Linear polyol; mannitol; polyo. pathogen resistance; salt stree inositol; ribitol; xylitol; ss 2000FR-00009032. 22-JUN-2001; 2001WO-FR001979. NEO; (first entry) al Similarity 59.2 831; Conservative (CNRS) CENT NAT RECH Noirand WPI; 2002-154933/20. WO200204647-A1 Beta vulgaris Lemoine RRP, 11-JUL-2000; 11-JUN-2002 17-JAN-2002 258 152 198 212 272 332 378 392 498 Query Match 438 452 Best Loca Matches 8

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ABL41873 standard; DNA; 2056

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Hybridisation assay, genetic mapping, gene expression control, protein identification, signal transduction pathway, metabolic pathway, promoter, termination sequence; ss.
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Score 470.2; DB 3; Pred. No. 5.2e-71; 1; Mismatches 559; 990S-0149923P.
990S-01499302P.
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990S-015066P.
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Length 1527; Indels

Query Match
23.3%;
Best Local Similarity 59.4%;
Matches 834; Conservative

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GTTCGCCTTCGCCTGCGCCATCCTCGCCTCCATGACCTCCATCCTCCTCCGGCTACGATAT GITCGCTTTCGGGTGTGCCATGTTGCTTCCATCTTTCTATCATCTTTGGATATGATAC GGTGGAGGTTCTCATGGGCATACTGAACCTCTACTCGCTCATCGGCTCTTCGCGGCGG GATTGAAGTTTTGGCCGGAATCTTGAATCTTTGTGCACTCGTCGGATCACTAACGGCGGG

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The present sequence encodes a polypeptide which is a transporter of a linear polyol. DNA encoding linear polyols is used to produce a selection system for transformed cells, based on the use of polyols as the only carbon source. It is also used to produce transgenic plants with increased resistance to pathogens and salt stress. The use of a linear polyol for selection eliminates the need for toxic selection reagents such as antibiotics. Also, the linear polyol is not essential for the plant, once selection has been made. The linear polyol has a main chain of 5.8, preferably 6, carbon atoms and is selected from sorbitol, dulcitol, galactitol, (myo-)inositol, ribitol, or xylitol
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New polyol transporter protein from plants, for selecting transformed cells and for imparting pathogen and salt-stress resistance to plants.
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pathogen resistance; salt stress; sorbitol; dulcitol; galactitol;
inositol; ribitol; xylitol; ss.
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Local Similarity 58.8%;
les 826; Conservative
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                                                                                           criecciricicacaraagarracaacacacacaccircrirricircacaagaarrac
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stress; sorbitol; dulcitol; galactitol.
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Pred. No. 2.1e-66;
1; Mismatches 544;
                                                                                                                                                                                                                                                     GGAGATGAGCAAGCTGTTCGGCGA 1555
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Matches 798; Conservative
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased colerance to ablocic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ1219-6-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to berwent by the European Patent Office
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Sequence 2378, Ap
Sequence 11442, A
Sequence 15, Appl
Sequence 4, Appli
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Sequence 1099, Appli
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GENERAL INFORMATION: 6383776
GENERAL INFORMATION: Steve
APPLICANT: Allen, Steve
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB-1163
CURRENT APPLICATION NUMBER: US/09/291,922
CURRENT FILING DATE: 1999-04-14
EARLIER FILING DATE: 1999-04-14
SERLIER FILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 2:
LENGTH: 2017
  US-09-606-421B-135
US-09-221-107-135
US-09-221-107-135
US-09-225-991A-11442
US-09-221-922-15
US-09-249-922-15
US-09-249-921-1099
US-09-130-114-2
US-09-130-114-2
US-09-130-114-2
US-09-130-114-2
US-09-130-114-2
US-09-103-840A-1
US-09-679-688B-15
US-09-103-840A-1
US-09-252-991A-1663
US-09-252-991A-16514
US-09-252-991A-15614
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100.0%; Score 2016.6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2017; Conservative 0; Mismatches
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    ; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-291-922-21
       RESULT 1
US-09-291-922-21
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Sequence 17, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 4731, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 27, Appli
Sequence 3960, Ap
Sequence 43, Appl
Sequence 43, Appl
Sequence 45, Appl
Sequence 1163, Appl
Sequence 11635, Apple 10536, Apple 10535, Apple 10
                                                                                                                                                           July 2, 2004, 02:27:34; Search time 173 Seconds (without alignments) 6470.150 Million cell updates/sec
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                                                                                                                                                                                                                                                           Description
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-162-012-45

US-09-252-991A-10535

US-09-252-991A-10535

US-09-252-991A-11395

US-09-252-991A-11395

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US-09-542-615A-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              682709 segs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        nucleic search, using sw model
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Maximum DB seq length: 200000000
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| 1292 | RESULT 4 US-09-21-922-27 US-09-21-922-27 US-09-21-1-922-27 Sequence 27, Application US/09291922 Sequence 27, Application US/09291922 Sequence 27, Application US/09291922 APPLICANT: Allen, Steve APPLICANT: Minney, Scott FILE REPERENCE BB-1163 CURRENT PELLIOR DATE: 1999-04-14 ERALLER PELLIOR DATE: 40-1998 SOUTH 180-12 US-09-29-92-27 ELANGER MICROSOFT OFFICE 97 ELANGER MICROSOFT OFFI OFFICE 97 ELANGER MICROSOFT OFFI OFFI OFFI OFFI OFFI OFFI OFFI O |
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CURRENT APPLICATION NUMBER: US/09/291,922 CURRENT FILING DATE: 1959-04-14 EARLIER APPLICATION NUMBER: 60/083,044 BARLIER FILING DATE: April 24, 1998 NUMBER OF SEQ ID NOS: 30 SEQ TWARE: Microsoft Office 97 SEQ ID NO 17
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US-09-291-922-17
$ Sequence 17, Application US/09291922
$ Patent No. 6383776
$ GENERAL INFORMATION:
$ APPLICANT: Allen, Steve
$ APPLICANT: Kinney, Tony
$ APPLICANT: Kinney, Tony
$ APPLICANT: Tingey, Scott
$ TILE OF INVENTION: Plant Sugar Transport Proteins
$ FILE REFERENCE: BB-1163
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Score 343.6; DB 4; Length 615;
Pred. No. 1.1e-58;
1; Mismatches 66; Indels 4:
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larity 50.1%; Pred. No. 3.3e-28;
Conservative 1; Mismatches 588;
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Allen, Stephen M.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: HEXOSE CARRIER PROTEINS
FILE REFERENCE: BB1160 US NA
CURRENT APPLICATION NUMBER: US/09/679,686B
CURRENT FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: MCCOSOft Office 97
SEQ ID NO 1
LENGTH: 1675
TYPE: DNA
CURRENT SCA mays
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NAME/KEY: unsure
LOCATION: (1624)
COTHER INFORMATION: n
FEATURE:
NAME/KEY: unsure
LOCATION: (1638)
COTHER INFORMATION: n
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LOCATION: (1668)
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; LOCATION: (1674)
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US-09-679-686B-1
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Sequence 1. Application US/09103840A

Patent NO. 6294328

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, OWEN R.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
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Pred. No. 3.4e-24;
1; Mismatches 597;
                                                                                        APPLICANT: Allen, Stephen M.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: HEXOSE CARRIER PROTEINS
FILE REFERENCE: Balled US NA.
CURRENT APPLICATION NUMBER: US/09/679,686B
CURRENT FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081,131
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1999-04-07
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Pred. No. 7.3e-19;
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                                                                           GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Allen, Stephen M.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: HEXOSE CRRIER PROTEINS
FILE REFERENCE: BB1160 US NA
CURRENT APPLICATION NUMBER: US/09/679,686B
CURRENT FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081,131
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1999-04-07
NUMBER OF SOD INOS: 24
SOFTWARE: Microsoft Office 97
RESULT 11
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; Sequence 17, Application US/09679686B
; Patent No. 6624343
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Patent No. 6624343
GENERAL INFORMATION:
APPLICANT: Allan, Stephen M.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: HEXOSE CARRIER PROTEINS
FILE REFERENCE: BB1160 US NA
CURRENT FILING DATE: 2003-01-16
PRIOR FILING DATE: 2003-01-16
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 24
SOPTIMARE: Microsoft Office 97
SEQ ID NO 9
LENGTH 1167
GCGGACCTGGTGGTG-----
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5.9%; Score 118; DB 4; I
Best Local Similarity 50.5%; Pred. No. 2.4e-14;
Matches 317; Conservative 1; Mismatches 301;
                                        3715465 Arcegogaaareerececececerarcreceeeceae
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US-09-489-039A-4762
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ORGANISM: 1
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Pred. No. 2.6e-15;
1; Mismatches 626; Indels
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APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: URAGER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN J.
TITLE OF INVENTION: TUBRECLUSIS
TITLE REPRENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
CURRENT FILING DATE: 1998-06-24
CURRENC OF SEQ ID NOS: 2.1
SEQ ID NO 2
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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OTHER INFORMATION: "n" bases at various
OTHER INFORMATION: represent a, t, c or
US-09-103-840A-2
                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
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ilarity 47.7%;
Conservative 1
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RESULT 14

US-09-489-039A-4762

US-09-489-039A

Sequence 4762, Application US/09489039A

Factor 10. 6610836

GENERAL INFORMATION:

TITLE OF INVENTION:

FILLE REPRENCE: 2709.2004001

CTRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

FRICE RAPPLICATION NUMBER: US 60/117,747

FRICE REPRENCE: 299-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 4762
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Job time : 199 secs
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patent No. 6551795

GENERAL INPORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 3992

LENGTH: 1344
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 21, App Sequence 21, App Sequence 19, App Sequence 19, App Sequence 27, App Sequence 21, App Sequence 28112, Sequence 78515, Sequence 26589, Sequence Seq US-10-437-963-87990 US-10-051-902-25 US-10-051-909-25 US-10-051-909-19 US-10-051-909-19 US-10-051-909-19 US-10-051-902-27 US-10-051-902-27 US-10-425-114-28112 US-10-437-963-78515 US-10-425-114-30135 US-10-425-114-26589 SUMMARIES Query Match Length DB Score 2016.6 1382.8 1094.6 1039.8 1039.8 1005 981.6 981.6 779.6 739.4 739.6 7 7 7 7 8 7 8 7 8 7 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 Result

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Sequence 21, Application US/10051902
| Sequence 21, Application US/10051902
| Publication No. US2002017468A1
| Publication No. US2002017468A1
| APPLICANT: Allen, Steve
| APPLICANT: Hitz, Bill
| APPLICANT: Tingey, Scott
| TITLE OF INVENTION: Plant Sugar Transport Proteins
| PILE REPERENCE: BB-116
| PILE REPERENCE: BB-116
| CURRENT APPLICATION NUMBER: US/10/051,902
| CURRENT PILING DATE: 2002-01-17
| PRIOR FILING DATE: BARLIER RAPLICATION NUMBER: US/09/291,922
| PRIOR FILING DATE: BARLIER FILING DATE: 1999-04-14
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Pred. No. 0;
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Best Local Similarity 100.0%;

Matches 2017; Conservative 0;
; LENGTH: 2017
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-051-909-21
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| APPLICANT: La Kosa, Tnomas J. APPLICANT: La Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei APPLICANT: Wu, Wei APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad | da o | 855 GTCCCCAAGAGGGAACGGAAACGAGAAGCGGTGTGAAGGAGCTCATCCTGTCCCG |
| Molecules and Other Molecules Associated With hereof for Plant Improvement 963 | 9 & 9 1 | 796 ACCCCGGCCAIGCGCGAAICGIGCICGCGGCGGCGGCCGCCTCCACIICIICAGCGCGCGGCGGGCGGGCGGCGGCGGCGGCGGCGGGCG |
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| re 1382.8; DB 17; Length 1897; dc. No. 0; Mismarches 263; Indels 27; Gaps 2; | QY QD | 1155 GGCGGGATAATCCTCTCCTCATCGGCCTCGGCGGCTCACCGTCGTCGCCAGCACACACA |
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                                                                                                                      Sequence 25, Application US/10051902
Publication No. US20020178468A1
| GENERAL INFORMATION:
| APPLICANT: Allen, Steve
| APPLICANT: Hitz, Bill
| APPLICANT: Hitz, Bill
| APPLICANT: Hitz, Bill
| APPLICANT: Hitz, Bill
| APPLICANT: Hinsy, Tony
| APPLICANT: Blands, Scott
| TILLE OF INVENTION Plant Sugar Transport Proteins
| TILLE REFERENCE: B8-1163
| CURRENT PRING DATE: EARLIER FILING DATE: 1999-04-14
| PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-04-14
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: Microsoft Office 97
| SEQ ID NO 25
| SEQ ID NO 25
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Best Local Similarity 79.1%;
Matches 1343; Conservative
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; ORGANISM: Triticum aestivum
US-10-051-902-25
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| 545 AACTTCGGCATCCTCCGGATATGTCTCCAACTTCGCCTTCGCCGCCTCTCCCTCC | 624 CTCGGGTGGCGCATCATGCTCGGCATCGGCGCGCGCCGTCCGT | 684 GIGCICGGCAIGCCGGAGICGCCGGGGGCGGTGGTCAIGAAGGGACGCCTCGCGGACGCC 743 [| 744 AAGGIGGIGCIGGAGAAGACCICCGACACGGCGGAGGAGCCGCGGAGGCCCTGCCCGAC 803 | 804 AICAAGGCGCCGCCGCATCCCTGAGGAGCTCGACGGCGACGTGGTGACCGTCCC 860 | 861 AAGAGAGGGAAAGGAAAGGGGGGTGTGGAAGGAGCTCATCCTGTCCCCGACCCG 920 | 921 GCCATGCGGCGCATCCTGCTGTCCGGCATCCACTTCTTCCAGCATGCGTTGGC 980 | 981 ATTCACTCCGTCGTCTTCTACAGCCCTCTCGTGTTCAAGAGCCCCGGATTAACGAACG | 1041 AAACACTTCTGGGGACCACTTGGCCGTTCGGTGACCAAGAGGCTTTTCATCTTGTTG 1100 1025 AGCCGTCTCCGGGGCACCACCGTGGCGGTCGGGGCCACCACAATACGGTCTTCATCTGTG 1084 | 1101 GCGACTTTCTTCATCGACGCGTCGGCGGCCGCTGTTGCTGGCAGGCGGGGGG 1160 | 1161 ATAATCCTCCCCATCGGCCTCGGCGGGCTCACCGTCGGCCAGCACCCGAC 1220 | 1221 GCCAAGATACCTTGGGCCATCGGCCTAAGCATCGCCTCCACCCTCGCCTACGTCGCCTTC 1280 . | 1281 TICTCCATGGCCTTGGCCCCATCACGTGGGTGTACAGCTCGGAGATCTTCCGGCTCCAG 1340 | 1341 GIGGGGGGGTGGTGGTCGGCGGCGAACGGGGTCACGGGGGGTCATC 1400 | | rcceccarcecceccrcecreegergrrrrranaactrccecenaacccecege 1 | | | 1641 CAAAATCACAAATCCTAAGGGTTTTCTTGCAAAAACGTGTGCTGTACTGGCTAGCTA |
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| ବପ | do Oy | 40 | AG QG | 장 | ර් යි | & 8 | \$ A | λο qq | S S | o S | Oy D | රු පි | , ço | ò d | Oy eg | ò 6 | oy Oy | |
| | Qy 1701 AAGTAGCAGCAACAAGAAGATTCGCTGATCCGGCGTTGCT 1745 | Qy 1746 GGAGAGCGACGGCGGC 1762 | RESULT 5 US-10-051-909-25 | ; Sequence 25, Application US/10051909 ; Publication No. US20020199217A1 ; GENERAL INFORMATION: ; APPLICANT: Allen, Steve | ; APPLICANT: Helentjaris, Tim ; APPLICANT: Hitz, Bill ; APPLICANT: Kinney, Tony ; APPLICANT: Tingey, Scott | ; TITLE OF INVENTION: Plant Sugar Transport Proteins ; FILE REFERENCE: BB1163 US CIP ; CURRENT APPLICATION NUMBER: US/10/051,909 ; CURRENT FILING DATE: 2002-01-17 | ; PRIOR APPLICATION NUMBER: 60/083,044 ; PRIOR FILLNG DATE: April 24, 1998 ; NUMBER OF SEQ ID NOS: 38 ; SOFTWARE: Microsoft Office 97 | ; SEQ ID NO 25 ; LENGTH 2089 ; TYPE: DNA ; ORCANISM: Triticum aestivum | 54.3%; Score 1094.6; DB 14; Length 20 79.1%; Pred, No. 1.1e-267; Tracle 18 | MACCHES 1343; COLLEGIVACIVE I, MISHACCHES 353; MACCHES 164 GCACCACCAAGAAGAAGGC 14 84 GCACCACCGGAGATGCTTCCGCCGCGCTGCCGGAGCCGTCGCCGCAAGAAGAAGGC 14 | | 204 TACGATATCGGGGTGATGGGGGCGTGCTGGCTGCTACATCAAGAAGGACTTCAACATCAGT 204 TACGATATCGGGGTGATGGGGGGGGCGTCGCTGACATCAAGAAGGACTTCAACATCAGT | | 324 GCGCCGGGCGCGCTCGGACGCGCCCCCCCGACGTGCTCGTTCGCCCCTCCCT | 384 ATATCTTCGCGGGGGGGGTTCCTCATCGGGTTCGCCGTCAACACACCCATGATTCTTCTTCTTTCT | Oy 444 GGCCGCTTCGTGGCGATCGGCGTGGGCTACGCGCTCATGATCGCGGCGGTGTACACC 503 | | 485 GGCGAGCGTCCCCCGCGTACGTCTCGAACTATGCTTTCTCCCGGCTTGCCGCTGAAC |

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US-10-051-092-19
Sequence 19, Application US/10051902
Sequence 19, Application US/10051902
Bublication No. US20020178468A1
GENERAL INFORMATION:
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Tingey, Scott
TILE OF INVENTION: Plant Sugar Transport Proteins
TILE OF INVENTION: Plant Sugar Transport Proteins
FILE REPRENCE: B8-1163
CURRENT FILING DATE: 2002-01-17
CURRENT FILING DATE: 2002-01-17
CURRENT FILING DATE: EARLIER FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
LENGTH: 1914
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US-10-425-114-30198
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Pred. No. 5.8e-239;
1; Mismatches 345; Indels 0;
                                                                                                                                                                                                                                  Sequence 27, Application US/10051909
Publication No. US20020199217A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Helentjaris, Tim
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Hinsy, Scott
ITILE OF INVENTION: Plant Sugar Transport Proteins
FILE REPERENCE: Bill 3 US CIP
CURRENT APPLICATION NUMBER: US/10/051,909
CURRENT APPLICATION NUMBER: 60/083,044
PRIOR APPLICATION NUMBER: 60/083,044
PRIOR APPLICATION NUMBER: 60/083,044
PRIOR APPLICATION OF SEQ ID NOS: 38
SOFTWARE: April 24, 1998
SOFTWARE: April 24, 1998
SOFTWARE: April 24, 1998
1628 AAGGCGAAAGTAGGGGAGATGAACTAGTGAGCTA 1661
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Best Local Similarity 77.4%;
Matches 1188; Conservative
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: DATE: 2021(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28112
LENGTH: 1704
TYPE: DAA
ORGANISM: Zea mays
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Pred. No. 1.3e-187;
1; Mismatches 405;
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US-10-425-114-28112
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| Query Match Best Local Similarity 7:04; Pred, No. 1:90-182; Indels 9; Gaps 1; Matches 992; Conservative 1; Mismatches 357; Indels 9; Gaps 1; Matches 992; Conservative 1; Mismatches 357; Indels 9; Gaps 1; 207 GATATCGGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGG | |
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Pred. No. 2.3e-177;
1; Mismatches 450;
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, OTHER INFORMATION: Clone ID: UC-OSFLCYP011G10_FLIUS-10-425-114-30135
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| CTTCTACACCTACCTCCCGGGAGACCCGGGAGGAGGA 1534 | and Other Molecules Associated With f for Plant Improvement 2_FLI 2_FLI 2_FLI 3-177; s 451; Indels 9; Gaps 1; s 451; Indels 9; Gaps 1; s 451; Indels 9; Gaps 1; s GarageGaraCorrect 163 GarageCaracararacacaracacaracacaracacaracacaracacaracacaracacaracacaracacaracacaracacaracacaracacaracacaracacarac | AIGIT 757 |
| Oy 1475 GCTCGCTGGGTGTTCTTCTACACCTACCTCCCGGAGACCCGCGGCCGGACGCT Db 1598 CGCAGGGTGTTCATGTACTTCTCTCCCGGAGACCCAAGAGCCT OY 1535 GATGAGCAAGCTGTTCGGCGACACGCCGCCTCGGAATCAGACGA 1582 Db 1658 CACCGTGAAGCTCTTCGGCAACGACGACGACGACGACGATGACGA 1705 | RESULT 14 US-10-123-114-2689 US-10-123-114-2689 PUBLICANT: Liu, Jingdong APPLICANT: Liu, Jingdong APPLICANT: Liu, Jingdong APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei TITLE OF INVENTION: Note of the Cac Electron Cooperation Note of the Cac Electron Cac Assistance Cac Applicant: Applicant: Cac Applicant: Applicant: Applicant: Cac Applicant | |

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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28469
LENGTH: 1777
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhatroidae; Oryza,
El (bases 1 to 804)
Satisauriyarat,C., Lu,G., Gawda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
Detween rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
BS721-0088, USA
Tel: 520 621 9288
Email: http://genome.arizona.edu
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CB620394 OSIIEB05J
CB621640 OSIIEB07K
CB625172 OSIIEB14C
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Copyright (c) 1993 - 2004 Compugen Ltd.
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EST 08-APR-2003

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CB678155 OSJUNEEOUX
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CG37639 OGDE44TV
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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Bhrhartoideae; Oryzeae; Oryza.

I (bases 1 to 788)

Jantaeuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

Fax: 520 621 9288
                                                                                                                                                                                                CB620394 768 bp mRNA linear EST 08-APR-2003 OSIIEa05J08.f OSIIEa Oryza sativa (indica cultivar-group) cDNA clone OSIIEa05J08 5', mRNA sequence.
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XhoI; Lesion Mimic SPL 11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           744 CCCGACGCCAAGATACCTTGGGCCATCGGCCTAAGCATCGCCTCCACCCTCGCCTACGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                         FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: K column: 22
Seq primer: gga aac agc tat gac cat g.
Location/Qualifiers
1. 804
/organism="Orya sativa (indica cultivar-group)"
/mol type="mRNA"
/culTivar="IR36"
                                                                                                                                                                                                                                                                                                                                                                                                   Score 796; DB 14; Length 804;
Pred. No. 2.6e-64;
0; Mismatches 5; Indels C
                                                                                                                                                                                                  /db_xref="taxon:39946"
/dlone="Collabo7K22"
/tissue_type="leaf"
/dev stage="3 week"
/lab_host="DH10B"
/clone_libe="OSIEB"
/note="Vector: pBluescript II
Xhol; Lesion Mimic SPL 11"
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.4%;
Matches 799; Conservative (
        PRimers
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ilarity 95.4%; Pred. No. 2.6e-61;
Conservative 0; Mismatches 38;
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les 786; Conser
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Best Local Si
Matches 786;
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae, Oryza,
1 (bases 1 to 824)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
Detween rice and Magnaporthe grisea
Contact: Rod Wing_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB621640 824 bp mRNA linear EST 08-APR-2003 OSIIEa07K22.f OSIIEa Oryza sativa (indica cultivar-group) cDNA-clone OSIIEa07K22 5', mRNA sequence.
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                                               TCTCATGGGCATACTGAACCTCTACTCGCTCATCGGCTCCTTCGCGGCGGGGGCGGACGTC
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0089, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: K column: 22
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
1. .824
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                                                           /mol_type="mRWA"
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/cult.var="IR18"
/clone="colife07K22"
/tiseur_type="Leaf"
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COMEDITY STATES TO MEAN SEQUENCE.

CEG78733.1 GI:29682458

EST.

CEG78733.1 GI:29682458

EST.

Cryza sativa (japonica cultivar-group)

EMCATYOTA, Viridiplantees, Streptophyta; Embryophyta; Tracheophyta;

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

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    Organism="Oryza sativa (japonica cultivar-group)" /mol_tryp="mRNA" /cultivar="Nipponbare"

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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, 95721-0088, USA
Tel: 520 626 3967
Fax: 520 629 9288
Email: http://genome.arizona.edu
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BACKWARD: gga aac agc tat gac cat g
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Seg primer: gga aac agc tat gac cat
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 818)
Jantasuriyarat, C., Lu, Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
Unpublished (2003)
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// mol type="maRNA"
// mol type="maRNA"
// do tref="taxon:39946"
// do xref="taxon:39946"
// clone="OSIEa4G12"
// tissue_type="Leaf"
// tissue_type="Leaf"
// dov stage="3 week"
// lab_host="DH10B"
// clone=lib="OSIEa4"
// noce="Woctor: pBluescript II KS +; Site_1: EcoRI; ShoI; Lesion Mimic SPL 11"
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Pred. No. 9.7e-60;
0; Mismatches 45; Indels
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O.
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BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: C column: 12
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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Matches 773; Conservative
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CD6723 Sativa (japonica cultivar-group) cDNA
Clone OSJNEe10K23 5', mRNA sequence.
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/dev_stage="3 week"
/lab_nost="DHIOB"
/clone_lib="0SJNEf"
/note="Vector: pBluescript II KS
XhoI; Uninfected Control"
xref="taxon:39947'
                  clone="OSJNEf01D24"
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/clone lib="OSJNEs"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after innoculation with Rice Blast (70-15)"
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                         Oryza sativa (japonica cultivar-group)

SM Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enthartoideae; Oryzeae; Oryza.

E 1 (bases 1 to 73)

Jantasuriyarat, C., Lu, G. Gowda, M., Hatfield, J., Zhou, B., Mazur, E. Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)
                                                                     Embryophyta; Tracheophyta;
1; Poales; Poaceae;
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    723
/organism="Oryza sativa (japonica cultivar-group)"

                                                                                                                                                                                                                                                                                                Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.8%; Score 722.6; DB 14; Length 723; 99.9%; Pred. No. 1.4e-57; ive 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                Box 210088,
                                                                                                                                                                                                                                                     Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O.
85721-0088, USA
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BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: K column: 23
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="makk"
cultivar="wipponbare"
db xref="taxon:39947"
clone="colNealok23"
fissue type="leaf"
dev stage="3 week"
lab_host="BHIOB"
                                                                                                                                                                                                                                                                                                                                                                           http://genome.arizona.edu
 GI:29678880
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                                                                                                                                                                                                                                                                                                                                  Tel: 520 626 3967
Fax: 520 621 9288
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KEYWORDS
SOURCE
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COMMENT
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CB678732 710 bp mRNA linear EST 09-APR-2003 OSJNEf01D24.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA clone OSJNEf01D24 5', mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae,
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GGTGTACACCGCCGAGGTGTCGCCGGCGTCGGCGTGGCTTCCTGACGTCGTTCCCGGA
                                                         121 GGFGTTCATCAACTTCGGCATCCTCCTAGGCTACGTGTCCCAACTACGCCTTCTCCCGCCT
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clade, Panicoldeae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGYBO78TH
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/clone="zmmBMa0642M1"
/clone_lib="zm 0.7_1.5 KB"
/reforcor: pBGSK-; Site 1: HincII; 0.7-1.5
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                                     Zhou, B., Mazur,
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 710)
Jantasuriyarat, C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 CACTCGACCGCCACTACTGTACACGGCCCAGAGCGAGCCTCCTCCTCCTCTGCACCACCG
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/mol type="mRNA"
/dolfivar="Nipponbare"
/db r=taxon:39947"
/clone="OSJNEf01D24"
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Pred. No. 5.9e-56;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DHIDB"
/clone_lib="0SJNB"
/note="Vector: pBluescript II KS
XhoI; Uninfected Control"
                                                                                                                                                                                                                                                                     FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 01 row: D column: 24
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                   Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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Best Local Similarity 99.7%;
Matches 705; Conservative
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AUTHORS
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Oryza sativa (indica cultivar-group)

ESM Oryza sativa (indica cultivar-group)

ENkaryorat, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae;

Ehrhartoideae, Oryzaa, Liliopsida, Poales; Poaceae;

Ehrhartoideae, Oryzaa, Oryza,

Is (bases 1 to 697)

S Jantaeuriyarat, C., Lu G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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/mol type="mRNA"

/mol type="mRNA"

/doutivar="IRS1"

/do xref="caxon:39946"

/clone="0SIIEa05H07"

/drssue_type="Lasf"

/dev stage="3 week"

/lab_host="DH10B"

/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: Xhol; Lesion Mimic SPL 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB620333 697 bp mRNA linear EST 08-APR-2003 OSIIEa05H07.r OSIIEa Oryza sativa (indica cultivar-group) cDNA clone OSIIEa05H07 3', mRNA sequence.
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                                                                                                  544 AICCIGCIGGIACGICICGAACIAIGCITICICCCGCIIGCCGCIGAACCICGGGGGG
                                                                                                                                                                         633 CGCATCATGCTCGGCATCGGCGCGCGCCGTCCGTGCTGCTCGCGCTCATGGTGGTCGTCGGC
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llarity 99.1%; Pred. No. 2.4e-54;
Conservative 0; Mismatches 6;
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Tel: 520 624 3967
Fax: 520 624 9288
Email: http://genome.arizona.edu
PCR_PRIMErS
FORMARD: gta aaa cga cga cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 65 row: H column: 07
Seq primer: gga aac agc att gac cat g
Location/Qualifiers
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943 324 883 384 823 444 763 504 703 564 643 624 583 684 523 744 463 804 403 861 343 921 283 981 223

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/clone="ZNMBMa0715N13"
/clone="LDE="ZN 0,7 1.5 KB"
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                    Length 1006;
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33.5%; Score 675.2; DB 29; Length
Best Local Similarity 80.2%; Pred. No. 2.7e-53;
Matches 804; Conservative 1; Mismatches 194; Indels
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1 (bases 1 to 106)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Rraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
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/organism="Zea mays"
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
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AU057756 Oryza sativa mature leaf Nipponbare Oryza sativa (japonica cultivar-group) cDNA clone S21759_1A, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spernatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
I (bases I to 700)
Yamamoto, X. and Sasaki, T.
Rice cDNA from mature leaf
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Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
GTGGAGGTTCTCATGGGCATACTGAACCTCTACTCGCTCATCGGCTCCTTCGCGGGGG
                                                                                         244 GIGGAGGITCICAIGGGCAIACIGAACCICIACICCCICCAICGGCICCTICGCGGCGGGG
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/dlone="821759_lA"
/tissue type="mature leaf"
/dlone_lib="Oryza sativa mature leaf Nipponbare"
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/cultivar="Nipponbare"
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Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantea; Srreptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantea; Srreptophyta; Embryophyta; Tracheophyta;

Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enthartoideae; Oryzae; Oryzae;

Enthartoideae; Oryzae; Oryzae;

Statasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,

Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

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Email: http://genome.arizona.edu
                                                                                                                                                                                                                                      CB620332 671 bp mRNA linear EST 08-APR-2003 OSIIEa05H07.f OSIIEa Oryza sativa (indica cultivar-group) CDNA clone OSIIEa05H07 5', mRNA sequence.
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      GAGATGGCTTCCGCCGCGCTGCCGGAGGCCGTCGCGCCGAAGAAGAGGGCAACGTCCGG 152
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/mol_type="mRNA"
/cultivar="IR36"
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Pred. No. 1.7e-51;
1; Mismatches 7; Indels
                                                                                       1162 TAATCCTCCCTCATCGGCCTCGGCCGGGCTCACCGTCG 1203
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XhoI; Lesion Mimic SPL 11"
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BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: H column: 07
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:39946"
/clone="OSIIEa05H07"
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/dev_stage="3 week"
/lab_host="DH108"
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Orgia sativa (indica cultivar-group)
Orgia sativa (indica cultivar-group)
Spermatophyta; Viridiplantae; Straptophyta; Embryophyta; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrarciophyta; Orgiae; Orgiae
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                                                                                                                                                                                                                                                                   1..68

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/dev_stage="3 week"

/lab_host="DH108"

/clone_lib="OSIIEa"

/clone_lib="OSIIEa"
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                          448A, P.O. Box 210088, Tucson,
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Pred. No. 8.3e-51;
0; Mismatches 6; Indels
University of Arizona
Biological Sciences West, 448A, P.O. B
85721-0083, USA
Tel: 520 624 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRIMETS
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: J column: 08
Seq primer: gga aac agc tat gac cat g
Location/Qualifiers
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CACCACTTGGCCGTTCGGTGTCACCAAGAGGCTTTTCATCTTGTTGGCGACTTTCTTCAT
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Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Other GSSs: PUJCW07TB
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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GG3DF74TV ZM 0.7_1.5_XB Zea mays genomic clone ZNATBMa0780N04,
GG260290
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citck, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Cohtact: Cathy Whitelaw
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/clone="zmMBM078N04"
/clone="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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Pred. No. 7.7e-51;
0; Mismatches 169; Indéls
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18-1: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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/organism="Zea mays"
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81.6%;
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CG064683 972 bp DNA linear GSS 19-AUG-2003 PUJCW07TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0639B13, genomic survey sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
I (bases 1 to 972)
Whitelaw, C.A.
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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9712 Medical Center Drive, Rockville, MD 20850,
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2, 2004, 08:27:21

Search completed: July Job time: 7796 secs

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/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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                                                                                                                                                Gaps
                                                                                                                                              3,
                                                                                                     Length 972,
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31.5%; Score 635; DB 29; Length 9
Best Local Similarity 79.1%; Pred. No. 1.3e-49;
Matches 768; Conservative 0; Mismatches 200; Indels
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

June 30, 2004, 18:24:42; Search time 59 Seconds (without alignments) 2456.727 Million cell updates/sec Run on:

US-10-051-902A-20 2559 1 MASDELAKAVEPRKKGNVKY......AEEAEDAAAKEKVVELPSSK 513 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* 1: genesecn1980~-Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | April 0.000 Beta | 35 Corn | 4 Wheat | 39 Wheat | 11 Rice B | 6 Rice | 13 Wheat | Abu08338 Wheat sug | . Aau97212 Soybean B | 7 Soybea | 9681 | 2072 Arabid | 2071 | 073 Arab: | _ | 3334 | Abp98504 PFAM cons | Aae35306 Human sug | Human | 935 Human | Aab66940 GLUTX2 co | Abg61548 Human tra | Aab66936 Rat GLUTX | Abu43281 Protein e | Aag15416 Arabidops |
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| ф | Query Match | 100.0 | 100.0 | 74.5 | 74.5 | 73.2 | 73.2 | 0.69 | 69.0 | 60.3 | 60.3 | 55.5 | 51.4 | 51.4 | 48.7 | 30.2 | 26.5 | 26.0 | 26.0 | 26.0 | 25.3 | 25.3 | 24.9 | 24.4 | 23.9 | 23.5 |
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| 26 | 27 | 28 | 23 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

RESULT 1 AAU97210

AAU97210 standard; protein; 513 AA.

the joyo

AAU97210;

(first entry) 27-AUG-2002

Corn Beta vulgaris-like sugar transport protein.

Corn; Beta vulgaris-like sugar transport protein; carbohydrate transport; grain filling; annual field crop; plant.

Zea mays.

US6383776-B1.

07-MAY-2002

99US-00291922. 14-APR-1999; 98US-0083044P. 24-APR-1998;

(DUPO) DU PONT DE NEMOURS & CO E I.

SV; Allen SM, Hitz WD, Kinney AJ, Tingey

WPI; 2002-453364/48. N-PSDB; ABK51971.

New nucleic acid encoding plant sugar-transport proteins, useful fo preparing transgenic plants with altered carbohydrate distribution.

Example 4; Fig 2; 54pp; English.

The present invention relates to the isolation of plant polynucleotide sequences encoding an Arabidopsis thaliana-like sugar transport protein or Beta vulgaris-like sugar transport protein. The polynucleotide sequences are useful for altering the level of sugar transport proteins in plants, i.e. for control of carbohydrate transport and distribution in plants, i.e. of uning grain filling of annual field crops (e.g. rrice, soybeans, and wheat), and, for studying carbohydrate flows and sigar transport. The polynucleotide sequences can also be used to isolate cDNA sequences and genes that encode homologues of the new proteins. The present sequence corn Beta vulgaris-like sugar transport protein

Sequence 513 AA;

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lant sugar transport proteins and nucleic acid encoding the useful for producing transgenic plants having altered levels
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N-PSDB; ABX93207.
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                 Length 513;
                                                    Indels
                 100.0%; Score 2559; DB 5;
100.0%; Pred. No. 3.1e-249;
ive 0; Mismatches 0;
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TINGEY S V.
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The present invention relates to the isolation of Arabidopsis thalianalike or Beta vulgaris-like sugar transport proteins, and the polymucleotide sequences encoding them. The plant sugar transport proteins of the invention have been isolated from corn, rice, soybean, and wheat. The polypeptides of the invention may be used for altering thevel of expression of a sugar transport protein in a host cell, by transforming a host cell with a chimeric construct encoding all, or a portion of the sugar transport protein, in sense or antisense orientation. Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants. ABU08334-ABU08339 represent Beta vulgaris-like sugar transport proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EILIGILSLYSLFGSFAGARTSDRIGRRLTVVFAAVIFFVGSLLMGFAVNYGMLMAGRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EILIGILSLYSLFGSFAGARTSDRIGRRLTVVFAAVIFFVGSLLMGFAVNYGMLMAGRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AGIPKGLDGDVVTVPGKEQGGGELQVWKKLILSPTPAVRRILLSAVGLHFFQQASGSDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQYSARLFKSAGITDDNKLLGVTCAVGVTKTFFILVATFLLDRAGRRPLLLISTGGMIVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MASDELAKAVEPRKKGNVKYASICAILASMASVILGYDIGVMSGAAMYIKKDLNITDVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MASDELAKAVEPRKKGNVKYASICAILASMASVILGYDIGVMSGAAMYIKKDLNITDVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGVGVGYGGMIAPVYTAEISPAASRGFLTTFPEVFINIGILLGYLSNFAFARLPLHLGWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMLAIGAVPSGLLALLVFCMPESPRWLVLKGRLADARAVLEKTSATPEEAAERLADIKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AGIPKGLDGDVVTVPGKEQGGGELQVWKKLILSPTPAVRRILLSAVGLHFFQQASGSDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LICLGSGLTVAGHHPDTKVAWAVALCIASTLSYIAFFSIGLGPITGVYTSEIFPLQVRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                  Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 2559; DB 6;
Best Local Similarity 100.0%; Pred. No. 3.1e-249;
Matches 513; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMGKLFGMPDTGMAEEAEDAAAKEKVVELPSSK 513
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The present invention relates to the isolation of Arabidopsis thalianalike or Beta vulgaris-like sugar transport proteins, and the polynucleotide sequences encoding them. The plant sugar transport proteins of the invention have been isolated from corn, rice, soybean, and wheat. The polypeptides of the invention may be used for altering the transforming a host cell with a chimeric construct encoding all, or a portion of the sugar transport protein in a host cell, by transforming a host cell with a chimeric construct encoding all, or a portion of the sugar transport protein, in sense or antisense or anticular and contentation. Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants. ABU08334-ABU08339 represent Beta vulgaris-like sugar transport proteins
                    419 ALGFAVGVASNRVTSAVISMTFLSLSKAITIGGSFFLYSGIAAVAWVFFFTCLPETRGRT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 QLEILIGILSLYSLFGSFAGARTSDRIGRRLTVVFAAVIFFVGSLLMGFAVNYGMLMAGR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein.
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                                                                                                                                                                                                                                                                                                                                                                                                 Beta vulgaris-like sugar transport protein; corn; rice; wheat; plant sugar transport protein; carbohydrate transport; soybean; carbohydrate distribution; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.5%; Score 1906.5; DB 6; Length 529; 73.6%; Pred. No. 2.7e-183; ive 58; Mismatches 71; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tingey SV;
                                                                                     505
                                                                                                                498 LEBIGKLFGMTDT--AVEAQDTATKDK
                                                                                   479 LEEMGKLFGMPDTGMAEEAEDAAKEK
                                                                                                                                                                                                                                   ΑĀ
                                                                                                                                                                                                                                                                                                                                                               Wheat sugar transport protein #5.
                                                                                                                                                                                                                                 ABU08339 standard; protein; 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Fig 2; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALLE/) ALLEN S M.
(HITZ/) HITZ W D.
(KINN/) KINNEY A J.
(TING/) TINGEY S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 373; Conserval
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N-PSDB; ABX93211
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14-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of plant polymucleotide sequences encoding an Arabidopsis thaliana-like sugar transport protein or Beta vulgaris-like sugar transport protein. The polymucleotide sequences are useful for altering the level of sugar transport proteins in plants, i.e. for control of carbohydrate transport and distribution in plant cells, e.g. during grain filling of annual field crops (e.g. corn, rice, soybeans, and wheat), and, for studying carbohydrate flows and sugar transport. The polymucleotide sequences can also be used to isolate cDNA sequences and genes that encode homologues of the new proteins. The present sequence represents a wheat Beta vulgaris-like sugar transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 WRVMLGIGAVPSALLALMVFGMPESPRWLVWKGRLADARAVLAKTSDTPEEAVERLDQIK 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLEILIGILSLYSLFGSFAGARTSDRIGRRLTVVFAAVIFFVGSLLMGFAVNYGMLMAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASDELAK--AVEPRKKGNVKYASICAILASMASVILGYDIGVMSGAAMYIKKDLNITDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding plant sugar-transport proteins, useful for preparing transgenic plants with altered carbohydrate distribution.
                                          Wheat, Beta vulgaris-like sugar transport protein, carbohydrate transport, grain filling, annual field crop, plant.
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  sugar transport protein encoded by wlml.pk0012.h1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.5%; Score 1906.5; DB 5; 73.6%; Pred. No. 2.7e-183; ive 58; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                               Kinney AJ, Tingey SV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Col 77-80; 54pp; English.
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Best Local Similarity 73.6'
Marches 373; Conservative
                                                                                                                                                                                                                                                                                                                                                               Allen SM, Hitz WD,
                                                                                                                                                                                                                                                                                                                                                                                                       2002-453364/48.
                                                                                                       Triticum aestivum.
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or Beta vulgaris-like sugar transport protein. The polynucleotide sequences are useful for altering the level of sugar transport proteins in plants, i.e. for control of carbohydrate transport and distribution in plant cells, e.g. during grain filling of annual field crops (e.g. corn, rice, soybeans, and wheat), and, for studying carbohydrate flows and sugar transport. The polynucleotide sequences can also be used to isolate cDNA sequences and genes that encode homologues of the new proteins. The present sequence represents a rice Beta vulgaris-like sugar transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU08336 standard; protein; 510
                                                                                                                                                                                                    60;
                                                                                                                                                                         73.2%;
72.7%;
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                                                                                                                                                                                      Similarity
                                                                                                                                                Sequence 510 AA;
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                                                                                                                                                                                                    372;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                 ALGFAVGVASNRVTSAVISMTFLSLSKAITIGGSFFLYSGIAAVAWVFFFTCLPETRGRT 478
                                                                                                                                                                                                                                                                                                                                                             497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta vulgaris-like sugar transport protein; carbohydrate transport; filling; annual field crop; plant.
                                                                                                                                                                             ACLIGLGTGLTVVGRHPDAKVPWAIGLCIVSILAYVSFFSIGLGPLTSVYTSEVFPRKVR
                                                                                                                                                                                                                                                                                                                                                 FVAGVGVGYGGMIAPVYTAEISPAASRGFLTTFPEVFINIGILLGYLSNFAFARLPLHLG
                                                                 FVTGIGVGYAIMVAPVYTPEVSPASARGFLTSFTEVFINVGILLGYVSNYAFARLPLHLS
                                                                                                        WRVMLAIGAVPSGLLALLVFCMPESPRWLVLKGRLADARAVLEKTSATPEEAAERLADIK
                                                                                                                                                             AAAGI PKGLDGDVVTVPGKEQGGGELQVWKKLILSPTPAVRRILLSAVGLHFFQQASGSD
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/label= Unknown
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                                                                                                                               GCSLGVAANRVTSGVISMTFLSLSKAITIGGSFFLYSGIAALAWVFFYTYLPETRGRTLE
                                                                                                                                                                                                                                                                                                              AGIPEELDGDVVTVP-KRGSGNEKRVWKELILSPIPAMRRILLSGIGIHFFQHALGIHSV
                                                                                                                                                                                                                                                                                                                                         VQYSARLFKSAGITDDNKLLGVTCAVGVTKTFFILVATFLLDRAGRRPLLLISTGGMIVS
                                                                                                                                                                                                                                                                                                                                                         300 VFYSPLVFKSPGLTNDKHFLGTTWPFGVTKRLFILLATFFIDGVGRRPLLLGSTGGILLS
                                                                                                                                                                                                                                                                                                                                                                                                               GFAVGVASNRVTSAVISMTFLSLSKAITIGGSFFLYSGIAAVAWVFFTCLPETRGRTLE
                                                                         VMLAIGAVPSGLLALLVFCMPESPRWLVLKGRLADARAVLEKTSATPEEAAERLADIKAA
                                                                                                                                                                                                                                          LICLGSGLTVAGHHPDTKVAWAVALCIASTLSYIAFFSIGLGPITGVYTSEIFPLQVRAL
                                                        1 MASDELAKAVEPRKKGNVKYASICAILASMASVILGYDIGVMSGAAMYIKKDLNITDVQL
                                                                                                              EILIGILSLYSLFGSFAGARTSDRIGRRLTVVFAAVIFPVGSLLMGFAVNYGMLMAGRFV
                                                                                                                                                                      AGVGVGYGGMIAPVYTABISPAASRGFLTTFPBVFINIGILLGYLSNFAFARLPLHLGWR
                                                                                                                                                                                                                                                                                    AGIPKGLDGDVVTVPGKEQGGGLQVWKKLILSPTPAVRRILLSAVGLHFFQQASGSDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta vulgaris-like sugar transport protein; corn; rice; wheat; plant sugar transport protein; carbohydrate transport; soybean; carbohydrate distribution; plant.
                            ë,
Score 1872.5; DB 5; Length 510;
Pred. No. 7.1e-180;
0; Mismatches 77; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMGKL/FGMPDTGMAEEAEDAAAKEKVVELPSS 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice sugar transport protein #3
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Rice; grain Oryza

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The present invention relates to the isolation of plant polynucleotide sequences encoding an Arabidopsis thaliana-like sugar transport protein

nucleic acid encoding plant sugar-transport proteins, useful for paring transgenic plants with altered carbohydrate distribution.

N-PSDB; ABK51972

Example 4; Fig 2; 54pp; English.

preparing

New